

FIGURE 1

ACTGCACCTCGTTCTATGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCACCGCGTCCGGGCCGGAGCACGCCGCAGGACCTGGAGCTCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCCTGCCGCCGGAGGCCAAAGAACGCCACGCCCTGCCACCGGTGCCGGGGCT
CTGCTGCCGCCGCCGGAGGCCAAAGAACGCCACGCCAAAGAACACTTGGCGGCCGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCGTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCACTTCAATGCAATCAGATGCTAGAGGCCAGGAGGA
GCACCTGGAGGGCTGGTGGCTGAGCTGAAGAGCAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGAATGCCACTGCAAGCGGAGATGGGAGCAGACA
GGGCAGGGTCTGCCGGTCCACATGGGTACAGGGCCCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACAGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGAAGACGTGCTCGGCCCTGACCAACAGAGACTGCGGCAGTGTGAAGTGGGCTGGTGCT
GGACGAGGGCGCTGTGTGGATGTGGACGAGTGTGCGGCCAGGCCCTCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCTACAGTGCAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAACG
AAAATGCTACAAACTCCAGGGAGCTACGTCTGTGTCTGACGGCTTCGAAGAACG
GAAGATGCCCTGTGCGCCGCCAGGGCTGAAGGCCACAGAAGGAGAAAGCCCACAGCT
GCCCTCCCGCAAGACCTGTAATGTGCCGACTTACCTTTAAATTTCAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGCTCTGCAGTGGACAGCGGGGGAGGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTGTATATTTGATACAGTCTTGTATAAAAATTGACCATTGAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAGGGCGCCGCGACTCTAGAGTCACCTGCAGAACG
TTGGCCGCCATGGCCAACCTGTTATTGCACTTATAATGGTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTTCACTGCATTCTAGTTGTGGTTGTCAAACCTC
ATCAATGTATCTTATCATGTCGGATGGGAATTAAATTCCGCCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGGGAAAGAACCCAGCTGTGAAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T) : 2

MRLPRRAALGLLPLLLLPPAPEAKKPTPCHRGRGLVDKFNQGMVDIAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDPECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLAQGGQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPCTDCMDGYFSSLRNEHTSICTACDESCKTCSGLTNRDCGECEVGWLDE
GACVDVDECAAEPPPSCAAQFCKNANGSYTCCEEDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAAGGTCCAAC TG CACCT CGGTT TAT CGATT GAA TTCCC CGGG AT CCT CTAG AGA GAT CCTC
GACCT CGAAC CCAC CGCGT CC CGG CAGGG CGGC ACG CGCC AGCGT CCT AAAC CGGG AA CA
GCCCT GGG CTG AGGG AGC CTG CAG CGC AGAG TAT CTG ACAG CGC CAG GT CGTAG GT CGC
GCAC GAGG AGT T TCC CGG CAG CGAG GAGG TCT GAG CAGC ATGCC CGG AGG AGC GCG CCT
CTT GCG CGC GCT CTG CTG GAG CAT CCT CCT GTG CTG TGT GG ACT CGGG CGG AGG C
CGGG CGC CGG CAG GAG GAG CGCT GAG CCT GTG ACCT ATGG ATG GTC CCT AGC CAGG
TAGG ATT TG AAGA AGA ATAT CCT GTT AGG TCT CGAG GGG AAAT AGG CAC TT TAC ACAT G
TTCAG AAA AG CGC AAC AGA ATG CGC AGC TAT CCT GTCA AT AAT CCT CAT GA ATT TAC
CTGG CAA CTG CAG GGC AGG CAG A ATACT TCT ATG AAT TCC CTG CTC TTG CGC CCT CGG ATA
AAGG CAC TAT CGG CAG ATC AAC CGT CA ATG CCT CTG CGT GGG AAAC AGC TGC CT CAA AGG CA
TCAGT GTT CAAG GTG TT CCC ATG CT GTT CGG AAA AC CAG AT GGG GT CGC AGC ATT TAAGT
GGAT GT GAT GTT ATG AAT TCT GAGG CAA CAC CATT CCT CAA AAC CCT CAA ATG CT AT CCT
TCT TAA AAC ATG CTG CAA AC AGT CGAGT GGC CAGG CGGT GCG GAA AT GGAG GCT TTT GT AAT
GAAAG AGC C AT CTG CGAG T GT CTC TGT GGG TCC AC CGG AC CCT CACT GTG GAA AGG CCT TTG
TACCC CAC GAT GT ATG AAT GTG GCA TTT GTG GACT TT GTG CACT GTG TTT CTG C AT CTG CCA AC TG
GATT CT AT GG AGT GAA CT GT GACA AAG CAA ACT GT CTA ACC AC CT GT TTA AT GGAG GAG C
TGTTT CT ACCT CGG AAA AT GT ATT TG CCG CCT CAG GAG TAG AGGG GAG AGC ACT GTG AAAT CAG
CAA AT GGC CCA AAC CCT GTG CGA ATG GGAG TTA ATG CTA GTG TAA AGC CAA AT GT AAG GTT
CCAA AGG TT ACC CAG GGAG AC CCT GTT CA AGG CTG TCG GAG CCT GTG GTG CAC AT
GGAA AGC CTG CCA TGA ACC CAA AT GCA AT GT CTA AGG AAG GT TGC AT GG AAG AC ACT GCAA
TAAA AGG TA CGA AGG CAC CCT CAT ACAT GC CCG TAG GGC CAG CAG GCG CCT GCA CGC
ACAC GCG CCT TCA CT AAA AGG CCG GAG GAG CCG CGG GAT CCT GAC AT CAA AT CATT AC TCG
TGAACT CGC ACAT CTG CAA AC GTT TAAGT TAC ACCA AGT TCA TAG CTT GTT AA CCT TTCA
TGT GTG TA AGT GTT CAA AT TAAT GTT CATT AC TA CCT AGG AA AT TCA CTG GCT GAA ATT TT ATT AGCT
CT ATT TAAT AAT ACT CAG GCT GT AT TTT ACT CCT TT TAAG TTT CT AAG TTT CT AAG TAC GT CTG TAG
CAT GAT GG TAT AGAT TT TCT GTT CAG TGT TT GGG CAG A GAT TTT AT ATT ATG TCA ATT GT
TCAGG TTT AAA ATT TT CAG TGT GT AGT TT GGC CAG A GAT TT TCA AA ATT ACA ATG CATT AT GGT
GT CT GGGGG CAGGG AA ACAT CGA CAA AGG TT AAAT TGG CCA AA AT GCG TAAGT CCA AAGA AT
TTGG TGT GCG CAG TTA AT GTG AAGT TAC CAG AT TT CAG AT TT TAT GTG CAG AT ATT TAG AT
GTT GTT AC AT TTT AAA ATT GT CTT AAT TT TTA AAT CTC TA AAT CAA AT AAT ATT TT GAC
TT CAC ATT ATT CCT CAG AGAT T CAG TTA AAA AAA AAA ATT AC TGT GTG TAG TGC CATT
AAAC AAT AAT AAT ATT CCT AAC CA AT GT AAT AGG GAA AT TAAT GT AAT GCA ACT TT GCG CAT
TGG CTT GAAG CAA TAT AAT ATT GT AAT AAC AAA AAC CAG CT TCT ACT CAA TA AAT CATT
ACT GT TT GT AT GT TAA AAA TA AAG GT GT GCT GT CTT TAG TTT GTG AAA AAA AAA AAA AAA
AAA
CGGC AT GGC CCA ACT GT GT TTT ATT GTG CAG CTT TAA ATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNINHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPCHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CCGGACGCGTGGCGTCGGCGGTGCAGAGGCCAGGGCGAGGCCAGGGCGCAGGCCAGCTGGG
CCCCAGCCCACACCTTCAACAGGGCCAGGCCAC**ATGTGGCGATGTCACTGGGGCTAC**
TCTGTTGCTGCCCTGGCTGCCACTTGCCTCTGGTGCAGCAGGGCTGGCCGG
GAGCTAGCACCGGGTCTGCACTTGCAGGGCATCCGGACCGGGAGGCCGTACTGCCAGGA
GCAGGACCTGTGCTGCCACCCCTTTCCCCGATCCAAGGGATGTATGCATGGAGGTGTATCTA
GTACTGTGACCTTCTGCAACCGCACGGTCTGGACTGTGCTGCCCTGACTTCTGGACATTCT
TGCTCGCGTGCACCCCTTTCCCCGATCCAAGGGATGTATGCATGGAGGTGTATCTA
TCCAGTCTTGGGAACGTAACGGACAACGTAAACGGTGCACCTGCCAGGAGAACAGGCAGT
GCCATGGTGGATCCAGACATGATAACAGGCCATCAACAGGGCAACTATGGCTGGCAGGTGG
GAACACCAGGCCCTCTGGGCATGACGGTGA**CAGGGCATTCGCTACCGCCTGGCACCA**
TCCGCCCATCTCTGGTCATGAAACATGCCATGAAATTATACAGTGTGCTGAACCCAGGGAG
GTGCTTCCACAGCTTCGAGGCCCTGTCAGGAAAGTGGCCACCTGTGATTCTGATGACCTTGA
CCAAGGCAACTGTGCGGGCTCTGGGCTTCTCACAGCACGTGTCATGGCAGTGTCT
CAATCATTCTGGACACATGACGCCCTGTCCTGTGCCCCAGAACCTGTGTCTTGAC
ACCCACAGCAGGGCTGCCGGTCTGGATGGTGTGCTGGCTTCTGGCTCG
CCGAGGGGTGGTGTCTGACACTGCTACCCCTCTCGGGCTGTGAACGAGACGAGCTGGC
CTGGCCTCCCCCTGTATGATGACACAGCGGAGCATGGTCTGGGCAACGGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTATAAACATGACACATCTACAGGCTACTCTGTCTACCGCCT
CGGCTTAAACGAGGGAGATCATGAAGGGCTGTGGAGAATGGCCCTGTCCAAGGCCCTCA
TGGAGGTGCTGAGGACTTCTCTTACACAGGGAGGCACTACAGGCCACAGCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCACTCAGTCAAGATCACAGGATGGG
AGAGGAGACGCCAGGAGGACCTCAAATACTGGACTGCTGCCACTCTGGGCC
CAGCCTGGGGCAGAGGGCCACTTCCGCTATCGTCGGGCTCAATGAGTGCACATCGAG
AGCTTCTGTGCTGGCGTCTGGGCGCTGGGATCATGGGCTACTGGGTCTACACTGAGGCTG
CGGGCCACAGGGGGTCCGGCTCAGGGCTAAGGGCTGGGGCGGAAGAGGCCCAATG
GGGCGGTGACCCCCAGCCTCGGGACAGAGCCGGGCGCAGGGCGGCCAGGGCTTAAT
CCCGGCCGGGTTCTGGCTGACCGCAGGCCCGCTGGGACGCCGGGCCAGGGCTAAT
GAGCCCCCAGACCTCCCACTGGGACGGGCCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGGCCTCTGGCGCCCCACTCAAGACTACCAAGGAGCACCTCAAGTCTCCAGC
CCCAATACCCCAACCCCAATCCCGTATTCTTTTTTTAGACAGGGTCTTGTCTCCG
TTGCCCAAGGTTGGAGTGCAGTGGCCATCAGGCTCACTGTAACCTCGACTCTGGGTCA
AGTGACCCCTCCACCTCAAGTAGCTGGACTACAGGTGACCCACACCTGGC
TAATTTTTGTATTTTTGTAAAGAGGGGGCTCTACTGTGTGCTCCCCAGGCTGGTTTCAACT
CCTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGGATIGCAGGCATGAGC
ACTGCAACCCAGGCCCTGTATTCTTACAGATATTTATTTTCTTCACTGTTTAAAAA
TAAAACCAAAAGTATTGATAAAAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCCRGRADDCA
ALPYLGAICYCSDLFCNRDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLAGWEPQRLLGHDPG
CTCQENRQWHGGSRHDQSHQPGQLWLWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTACACAGCAAGCTNTGCNATCCGATTGTTGTCTAAATCCA
ATTCTCTGGGACACATNACGCCCTGCTCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCTGGTGGTGGTCTGCGTCGCCGAGG
GNTGGTGCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCAGGCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGA~~T~~CTGCCTGCAGGTGGAGAA~~T~~CTGCACCCAGCTGGG
GAGCAGTGCTGGACCGCGCCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTGAACTCGTGG~~A~~TGCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCTGCTGCTCTGGGACC~~C~~GGCCAGCTATAGGCTCTGGGGG
CCCCGCTGCAGCCCCACACTGGGTGTGGT~~G~~CCCAAGGCCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGGTGGGAGCCTGCTGGTCC~~T~~GGAGGCACATCTTAACGCAAGTCTGACCATGATGT
CTGCACCCCTGTCCCCCACCC~~T~~GACCC~~T~~CCATGGCCCTCTCCAGGACTCCCACCCGGAGA
TCAGCTCTAGTGACACAGATCCGCC~~T~~GAGATGGCCCTCCAACCC~~T~~CTGCTGCTGTTTC
CATGGCCCAG CATTCTCCACCC~~T~~TAACCC~~T~~GCTCAGGACACTCTTCCCCCAGGAAGCCTT
CCCTGCCCA~~CC~~CCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCG~~C~~ACCCAGCA
GGGGACAGGC~~A~~CTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAA~~CT~~GG
GGACAAGAGTCGACGTGAGTTCC~~T~~GGAGTCTCCAGAGATGGGGCCTGGAGGC~~T~~GGAGGAA
GGGGCCAGGCC~~T~~CACATTG~~T~~GGGGCTCC~~T~~GAATGGCAGCCTGAGCACAGCGTAGGCC~~T~~T
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLPVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPAPFSTLNVLRLHFQEAFFPAHPYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACCGTCCGAACCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGCGCATGACC
GACCAGCTGAGCAGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGC
CGTGCAGGTCACCGGGCGTCGCATCTCCGCACCGCGAGGACGGACAAGTTGCCAAGC
TCATAGTGGAGGACGGACAGCTTGGCAGCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGAAGGCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATA CGGCCCTTCAGAACGCCCGCACGAGG
GCTGGTTCATGGCCTTCACCGGGCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGGCCGAGGGCCACTTCATCAAGGCCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGCAGAACGAGCTTCAGTTGTGGCTCCGCCACCGCGGACCAAGGCCACAC
GGCGCCCCCAGCCCCTCACCTAGTCTGGAGGCAGGGCAGCAGCCCCCTGGCCGCCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGAAAGGGCAGGGCGTG
CCCCAGGGCGGCTGGCACAGTGCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCACCCGTATCTCAGGCCACCGCTCTGCCGCCCTCCAGCCGGCTCCGTAAAGCC
CGCTGAAAGGTCAAGCAGACTGAAGGCCTTGAGACAAACCGTCTGGAGGTGGCTGTCCCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGCCCCAAACTCCTCCGGTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCACCCCTCACATTCCACGACCAGGCCCTGCACCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRQRQIREYOLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLIGKPSGKS KDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQKQFEF
VGSAPTRRTKTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

TATVKDQ-S226Q660

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGAAAGAGGCCAACACAGGCTGATAAGACCAAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTCGTTTATTTTTTTCTTTTCCACACATTGATTTC
TTCCGTACTTCAGAAATGCCCTACAGACCAAAAAGTGGCCAGCCATGGGCTTTTC
GAAGTCTTGCTTATCTTCCCCTGGGGCTACTCACAGGTGTCACAGGCTGACCTCAGTG
CTAGTGTGTGCGCTGCGACAGGAATTGTCTACTGTAAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAAACACCCAAATTAAATATGC
TGGATTTCCTGAGAACTGCACAAATGTACAGTGGTCGACACGGTCACCTGTATGCAACC
AACTGGACGAACTCCCATGAACCTTCCAAGAAATGTCAAGGTTCTCATTTGCAAGGAAAC
AATATTGACACCATTTACAGGGCTGCTCTGCCCCAGCTTGAGCTTGAGAGCTGACACCT
GGATGACAACCTCCATATCCACAGTGGGGCTGGAAGACGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAAGATCACCTGAGCAGTGTGCTGTGACATGGGCTTCTG
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCGACATGGGCTTCCAGAA
TCTCAGCAGCTGGAGGCGCTTATGTGGACGGGAAACCTCTGACCAACAAGGGTATCGCC
AGGGCACCTTCGACATCTCACAAAGCTAACGGAATTTCATTGTACGTAATTGCTGTC
CACCCCTCTCCCGATCTCCAGGTACGATCTGATCAGGCTCTATTGAGGACAACCGAT
AAACACAACTCTTGTGACGACGCTTCTCAATCTCGCTAAGTGGAAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTGATAATCTCCACACCTGAAAGCAGCTC
ACTGCTCGGAAATAACCTTGGTTTGACTGCTGAGTATTAAATGGGTCACAGAATGGCTCAA
ATATATCCCTCATCTCTCACGTGCGGGTTTGTGCAAGGTCTGAAACAAGTCCGG
GGATGGCGCTCAGGAATTAAATGTAATTGTTGCTCTGCCCACCCAGGACCCCGGCCCTG
CCTCTCTTCACTCCCGCCAGGAACTGACGCTTCTCCGACACTCAGCTCCACCCCTCTCAT
TCCAAACCCTAGCAGAAGCTACAGCCTCCAACTCTTACACATCGAAACTTCCACGATTC
CTGACTGGGATGGCAGAGAAAGACTGACCCCAACCTATTCTGAACGGATCCAGCTCTCATC
CATTTGTAATGATACTTCATTCAAGTCAGCTGGCTCTCTCTTCCACCGTGATGGCATA
CAAACATCAGGGTGAAATGGCCACAGTTAGTGGGGCATCTGTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACTGAGGCTGTTACTTAGAGCCCCATCCACCTATCGGATT
TGTTTACTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTTGTTCAAGGGC
CACCACCCATGCGCTCTTATCTGAACACGGCAGCAACACCGCTCCAGGACATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGGGCTGATGGGGCGCGGTGATATT
GTGCTGGTGTGCTTGTGCTCAGCGTCTTTGCTGGCATATGCCACAAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATAACCGGGCCCGGGAAAGATGATTATGGGAGCCAGGACACAGA
AGGACAACCTCATCTGGAGATGACAGAAACCAAGTTTCAAGATCTCTCTTAAATACGAT
CAACTCCCTAAAGGAGATTCAAGACTGCAAGCCATTACACCCAAATGGGGGATTAAATT
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGGCAGACCTGGAGC
ACTGCCATACGTGACAGCGAGGGCCAGCGTTATCAAGGGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACACCGCAGATTACATTGATAATGTTACAGATGCAT
TTGTGCAATTGAAACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATTTCTATTCAAGTAAACACAGTTGTAACTCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPSPHGAFFLKSWLIIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPPLGIP
EGVTVLYLHNQNINNAGFPAAELHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNDNSISITVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNNLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
DPGTHLIRLYLQDNQINHIDLTAFSNLRLKLERLDIISNNQLRMLTQGVFEDNLSNLKQLTARNN
PWFCDCSICKWVTEWLKYIPSSLLNVRGFMCGPEQVRGMARVELNMNLSCPTTTPLGLPLFTP
APSTASPTTQPPTTLSIPNPSSRSYTPPPTPTSKLPTIPWDGGRERVTTPPISERIQLSIHVN
TSIQVSVLSLFTVMAYKLTVVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVP
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAIVFLVVL
LSVFCWMMHKKGRTSQWKWYNRGRKDYYCEAGTKKDINSILEMETSFCIVSLNNNDQLLG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGGGCGCGCGGGAGACAGGGCAGAGGCAGAAGCTGGGCTCCGTCTTCGCCCTCCACGAGCG
ATCCCCGAGGAGGCCGCCGCCCTGGCGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCC
TCGCTCTCCAGGCCGCCGCCCTGGCGAGGCCAGAGGCCAGAGGCCAGAGGCCAGAGGCC
GCTTTCTGCTGATCTCGGAGCACAGTCGCTCTCCCTGGCGCTCTGCTGCCCTTGAAAATG
CTAGGGGCCAGACAGCTCGGACCCACCGCAGACGCCCTCTGGAGAGTTCTGTGAGAACAGCGGCCAGACC
TGGTTTCTCATTTGACAGCTCTGGCAGTGTGCAACACCCATGACTATGCAAAGGTCAAGGGAGTTCATCTGGACA
TCTGCAATTCTTGGCATTTGGCTCTGATGTCAACCCAGTGGGCCCTGCTTCAAATATGGCAGCACTGTCAAGAAATG
AGITCTCCCTCAAGAACCTTCAAGAGGAAGTCCAGGAGGTGGAGGCTGCTGCAAGAGGATGGGCATCTGTCACCG
GCACCATGACTGGGCTGGCCATCAAGTATGCCCTGAGCACATGCCATTCTCAGAGCAGAGGGGCCCGGCCCTGA
GGGAGAGATGTGCCACGGGTATAATGATCTGTGACAGATGGGAGACCTCAGGACTCTGGCCAGGTGGCTGTA
AGGCACGGGACAGGGCATCTAACTTCTTCCATTTGCGCAATTCTCAGGAGATGTGACAGCTGACCTCTGGTT
GGAGTGAGGCCATGAGGCCATTCTCTTCTGCGCAATTCTCAGGAGATGTGACAGCTGACCTCTGGTT
AGAAGAGGTGGCCAGGCCCATGTGCGACAGCTCTGGCAACCCCTGGAGCATAACTGTGCCACTCTGCAATCAAATCCCTG
GCTCATACGTCTGCAAGGCTCAATTCTCAACTCTGGCATAGCAGACTTGGCAGAATTCAGGAGATCTG
GTCCCATGGAGGACCAAACTGTGAGCAGCTCTGTGTAATGTGCCGGCTCTCTGCTGCTGCAACTG
GCTACGGCTCTGGAGGCTGGAGGAGGTGTGAGGCTACTGTGCTCAGAAAACACCGAGATGTGAC
ATGAGTGTGAAATGCTGATGGCTCTTACCTTGGCAGTGGCATGAAGGATTGCTTAAACCCAGATGAAAAAA
CTGCAACAGGATCAACTATGCTGCACTGGGGCTGTGAGCATGAGTGGCTCAACATGGAGGAGAGCT
ACTACTGCGCTGCCACGGCTCATCTGGACCCAACTCTGGCAACCTGCAAGGGAGTGGACACTGTG
ACGAGGAGCATGCTGTGAGCAGCTGTGCTGAAACAGGGAGATTCTTCGTCTGCCAGTGTCTGAGGCTTCC
TCATCAACAGGAGGCCATGCCGGGTGCTGGGCTGTGACTGGCTGAGTGGCATGACATGGTGAATACTCT
GIGTCAACATGGCAGATCTTGGCTCTGCTGAGTGTGCTGGAGCACCTGCTGCCACCGATGGGAGAGCTGTG
CAAATTTGAGCTCTGGCTCTGGGGCACACGGTGTGAGCATTCTGCTGTAAGCAGTGAAGGATTCTGGTTGT
GCCAGTGTGCTTGAAGGTTTATATCTCGTGAAGTGAAGAAAACCTGCGAGAAGGAAAGATGTCTGCAAGCTATAG
ACCATGCGCTGTGAAACACATTGTGTAACAGTGCAGCTCATACGTGCGAGTGTGTTGGAGGGATTCTCCGCTCG
CTGAGGATGGGAAACGGCTGCCAGGGAGGATGTGCAAACTTCAACCCCACCTGGCTGGCAACACATTGTGTTA
ATAATGGGAATTCTACATCTGCAATGCTCAGAGGGATTGTGCTGAGGACATCTGGCTGCAAGAAAT
GCACTGAGGGCCAATTGGACTCTTGTGATGTGATGCCAGGATCCAAGAGCTTGTGGAGAAGAGAATTGGAGGCTG
TGAGGAGCTTGTGCTGAGGATTATGATTCTGCAATTCTTCCCCCAAGCGCTGAGTGGGGCTGCTCCTAG
ATTCCACACAGGTCACACAGAGTCACTCTGAGAACCTTCAACTCAGGCCAACAGACATGAAAACGGCTGGCCC
ACATGAAAATCATGGGAAAGGCTCATCTGAGTGGCTGCCCTGAAACACATGTGTTGAGAGAATTCTACCCAG
GNGAAGGGGCCAGGCCCTTCCACAGGGTGCCCAGAGCAGGCCATTGTGTTCCAGGAGCAGGGCTCAGGAT
ACGTCTGGAGTGGGCCAGTGAAGATTAAGGAAAGCCAAAGGCAATTGGTACTATGTTGAGGTTGGGAGGAAAGGCCATTG
AGGAGGAATCTAACAGAGATTGGCTCTGAGGCCCAAACTCAACAGGATCTTGTGAGGCTCTAGAGAATCTCCAG
ATGAGATAAGTGAAGAAAACCTCAAGAGAAGGCTCTGGAGGCTCTAGAGAAGAGAATCTCCAGATGGAGACAGGACTCTCCAG
CAGGGGAATCTGCCAAACGGTCAACAGGCCAACAGGATCTGAGCAGTGCACCATTAATATCAGGAACTACTT
CTCTGTTCTAAATTGGCTGAGCAGATATCTGTTGAGAGAAGACATCTTACGGTCTACACAAAAGCTT
CCCCATTACACAAAACGGCTTACAGGAGGCCCTTGGAGAGAAAACAGGATCAATGCAATGAAATG
TCCAGAACCTTGCACAAAGGAAGAATGAGAAAATTACACAGGCCATTAGAAGAAATGACACAGAGATGGAGGCC
TGGAAAATCTGCCAGGATCAAGATGAGAATTGAGAATCTGGCAGCACATTGTGAGTCACTTGTGTTACCGGATTAACAT
GAACGGCAGTGCAGGGCCCAAAGCTCAGGTTATTGTTAAATCAATAATGTTGAGGTTAAAACATCAGTCTGA
GAAACCTGTTTGGCCACAGAAACAGAACAGAAGATTAACACTAATCTGTTGAGGTTATTGTTGAGGTTAAAACATCAGTCTGA
TAGAATTCTTAAGATGAAATTACAGGAGGAGATGAGTGTGAGGACTTACCTTGTGAGGACAC
AACTCTGCTCTGCCATCTGCCCTAGTGTGCAATCTTGTGACTTACCTTGTGAGGACTTACCTTGTGAGGACAC
CTGTTAGAACACTGGCCATAGGAAATGCTGTTTTTGTGACTTACCTTGTGAGGACTTACCTTGTGAGGACAC
CATAAATCATAGGAGCATATGTACTTGTGAGAACAGTTGGATTTTTATACAAATTTAAAATTCAACCTTCA

FIGURE 15

MEKMLAGCFLILGQIVLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFI
DSSRSVNTHDYAKVEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFLKTFRKSEVERAV
KRMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPVRIMIVTDGRPQDSVAEAAKARD
TGILIFAIVGQVFDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVADYCASENHGCEHECVNADGSYLCQCCHGFALNPDEKTCCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCRSRVDCLLSDHGCYEYSCVNMDRSFAQCPEGHVLRSDGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCSEGFLIREDGKTCRRDKVCQAIDHGCEHICVNSDDSYTCECLEGRFLA
EDGKRCRKKDVCKSTHHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIIDLSPKAARVGLLQYSTQVHTEFTLRFNFSAKDMKAVA
HMKYMGKGSMTGLALKHMFRSACQCPGEGARPLSTRVPRAAIIFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEEQEIASEPTNKHIFIYAEDFSTMDEISEKLKKGICAELEDSDGRQDS
PAGELEPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEDNLRLRSTQKLSHSTKPSGSPL
EKEHDQCKCENLIMFQNLANEVEVRKLTQRLEEMTQRMEALENRLRYS

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGGGCTGGCTCCCGCGCACGCTCCGGCGTGCAGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCGGCTGGCAGGGAGGGC
CATGATTTCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCACCGGGTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCCTCCAGCGTGGTACACCTGCAAGGGAGGTGCTTC
ATCCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAAGGAGGATC
AGGTGTTGTCATCATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCACTCC
ATGCCCTCCCGAACCTGCTCTGCGCTGGAGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGGAATGTGCAAGAACAAACAGGCAAATCTAGGGCCAAGCATCAAACCT
TAGAACTCAATGTAATGGTCTCCAGCTCTCCATCTGGCGTCTCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCCTGAGCTGCGCAGTCTCAAGGAGTAAGCCCTGTCCAATCCA
GTGGGATCGGCAGCTCCATCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGT
GGTCTTAAGCTACCAACCTTCTGCTCTCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAGTGAAGCACAGGGCTGGAGCTG
AGTGTGCTGGAGCTGTTCTGGGTACCTGGTTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTAACCACCGCGGGCAAGGGCCTGGAGGAGGCCAGCAATGATACTAACAGGAGGATGCC
ATTGCTCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCT
TTCTCTGTACCTCCGACAGGCCCTGGGCCACCCATGGCCCTCCAGGGCTGGTCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCACCTCAACCAATATCCCCATCCCTGGTGGGTTCTCTCTGGCTTGAGCCG
CATGGGTGCTGCGCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCCTGAGTCATGGAAAGAGTCACACTCTGACCCCTAGTACTCTGCCCAACCTCTC
TTTACTGTGGAAAACCATCTCACTAACAGCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGAAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTTATGAAGGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAAAACTAACATGAAATATGTGTTGTTCTTTGCAATTAAATAAGATACATAA
TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKDQVLSYINGVTTSKPGVSLVYSMPSRNLRLLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNCVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEADIAPIRTPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPPSLSSQALPSRPLPTTDGAHPQPISPPIPGGVSSSGLSR
MGAAPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCCCACTGGGCCACGCCAATGAAACGCCCTCCCGCTCTAGTGGTTTTCCACTTTG
TTGAATTGTTCTATACTCAAAATTGACCAAGACACCTTGCTCCCAAATGCAAATGTGA
AATACGCAATGAAATTGACCGCTGCTATTGCAACATGGATTTCAGGAAATGGTGTACAA
TTTGAGAGATGATAATGAGTGGAAATTAACTCAGTCTGTGGCGAAATGCTAATTG
ACTAACACAGAAGGAAGTTATTGATGTGTGACCTGGCTTCAAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCGCTGTGATAGAAAATGTGAATGCAAATGCCCCATT
TAGATAATGCTGTATAGCTGCAAATATTAAATAAAACTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGTCTACAAGAAGTCTAGAGAAAATCTGTGACAGATCTTCAACAAACAGA
TATAATTACATATAGAAAATTAGCTGAAATCATCTCATTACTAGGTTACAAGAACACA
CTATCTCAGCAAGGCACCCCTTCTAACCTCAACTCTTCAACTGAAATTGAAAAACCGTGAAT
AATTGTTCAAAGGGATACTTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTCAAAACTCATGCACACTGTTGACAAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCCACAGGTTGATCAAATTCAGGATTAAGCTCTCAAAGTTTCTTTTGAT
TCATATAACATGAAACATATTCTACCTCATATGAATATGGATGGAGACTACATAAATATATT
AGAGAGAGAGAGAGAGCTGCAATGATCAATTGCAATGGTGTGAGTTGATTTTATTTATA
AGAGTATTGGTCTTGTCTCATCTGACAACCTCTTATTGAAAACCTCAAATATGAT
AATTCTGAAGGGAGGAGGAAAGAGTCATATTCTCTGAGTCAATTCTAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACTTGGAAAAAAATACATTACATTAAGTCATCGAAAGGTCAACAGATA
GGTAGGAGTCTATGTGCTATTGGAAATTACTCACCTGATCATGAAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATCAACTAACATGAGACCCACACTCATGCCCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCTCTCCATTGGTATTAAAGATTATAATTCT
TTACAAGGATCACTCAACTAGGAATAATTATTACTGATTGCTTGTCCATATGCAATTTT
ACCTCTGGTCTTCAGTGAATTCAACAGCACCAGGACAACAAATTCAAAAAATCTTGCTG
TAGCCTATTCTCTGCAACTGTTCTCTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCGGACTGCTACACTACTCTTTAGCTGCTTTGCTGGATGTG
ATTGAAGGCATACATCTCATCTCATGGTGTGGTGCATCTACAAACAAGGGATTGGCA
CAAAAGTTTATATCTGGCTATCTAACGGCCAGCGTGTGAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTGGCACAACCAAGTATGGCTTAGCACCAGAAAACAACCTTATT
TGGAGTTTATAGGACAGCATGCTTAACACTATTCTGTTAATCTTCTGGCTTTGGAGTCAT
CATATACAAAGTTTCTGCAACACTGCAAGGGTTGAAACCCAGAAGTTAGTTGCTTGGAGACA
TAAGGTCTGTGCAAGAGGGCCCTGCTTCTGTTCTCTCGGCCACACTGGATCTT
GGGGTTCTCCATGGTGTGCAAGCTGTTGAGCTTACCTCTTCAAGTCTGAGCTG
TTTCCAGGGGATGTTCAATTCTCTGTTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAATGTCCTCTGTTTGGATGTTAAGGTAAACATAGAGAATG
GTGGATAATTACAACCTGCACAAAAAATAAAAAATCCAAGCTGTTGAGTACCAATGTATAAAAAA
TGACTCATCAAAATTCCAAGTACTAGACAAAAAGTATTAAATCTGATCATATAGATACATG
TTTCTATGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCCAAAGGAAGATTCTTCTAACACGAGAAGTATGAA
TGTCTGAAAGGAACACTGGCTTGTGATATTCTGTGACCTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGGTAATGACCTCATTACAGAAAGTGGACATAAGAGAATGAAAGGGCAGA
ATATCAAACAGTGAAGGGAAATGATAAGATGTATTGAACTGTTTCTGAGAC
TAGCTGAGAAGAATTGTTGACATAAAAGAATTGAAAGAAACACATTACCCATTGAA
TTGTTCTGAACTTAAATGTCCTAAACACTTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENACTNTEGSYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCAA
NINKTLTKIRSIKEPVALLQEVRNSVTDLSPTDIITYIELAESSSLLGYKNNTISAKDTL
SNTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHTKLMHTVEQATLRIQSFSQKTTEFDT
NSTDIALKVFVFFDSYNMKGHHPHMNNMDGDIYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPONYDNSEEERVISSVISVMSNPPTLYELEKITFTLSHRKVTDYRSILCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRCHNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIYQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSIIAGL
LHYFFLAFAWMCIEGITHLYLIVVGVIYNKGFLHKNFYIFYGLSPA VVVGFSAA LGYRYGT
TKVCWLSTENNFIFS FIGPACLI ILVNLLAFGVII YKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATTAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTTGATGTCCTCTGGCTTCCATTGGTATTAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTGGGGCCCGTCGCGCGTGGGGAGGGAGTTCCCGAAACCCGGCCG
CTAACGGAGGCCCTCCTCCCGCAGATCGAACGGCCTGGCGGGGTCACCCCGGCTGGGA
CAAGAAGCCGCCGCCTGCCTGCCCGGGCCGGGGAGGGGGCTGGGGCTGGGGCGGAGGCCG
GGTGTGAGTGTTGCTGCGGGGGCGAGGCTTGATGCAATCCGATAAGAAATGTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGGCGCTACTATATAAGGCTGCGGGCCCGGAG
CCGGCGCGCCCTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGCAGCGCATCCCGTGCAGCCAGCCTCCGCACCCCATCGCGG
AGCTGCGCCAGAGGCCCCAGGGAGGTC**CATGCGAGCGGGTGTGTTGTTCCACG**TATGG
ATCCCTGGCCGCGCTCTGGCTGGCGCCGGGCCCTCGCCTTCGAGCGGGCC
CCACGTGCACTACGGCTGGGGCAGCCCCATCCGCTGGGACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTCGCAGTCCGGAGCGCTGTGGACTGCGCGCGGGC
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCACTGCTGCGGACCGCTGGGACATCAAGGG
CGTGCACAGCGTGGGTACCTCTGCATGGCGCCAGCGAACGATGCAAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCGGAGAAGCACCGCCGGCTCCCGTCCAGTGGCAGCTGCAAAACAGCGGAGCTGACAGAA
CAGAGGCTTCTCCACTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTCTGCCCTGGAGACCGACCATG
GACCCATTGGCTTGTCAAGGACTGGAGGGCCGTGAGGAGTCCAGCTTGAGAAG**TAAC**
GAGACCATGCCGGCTCTTCAGTGTCCAGTCTGTTAGCTGGTACCTGAGCGTGGGAGC
TGCTCTACAAAGAACAGTCTGAGTCCAGTCTGTTAGCTTAGGAAGAAAACATCTAGAA
GTTGTACATATTCAAGAGTTTCATTGGCAGTGCAGCTTCTAGCCAATAGACTTGTCTGAT
CATAAACATTGTAAAGCCGTAGCTTGGCCAGTGTGCTGGCTGGGCCCATCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACCTCTTGGAAAATTTCTTATGTCAGCTGAAATTCTCATCTAAATTCTCATCTTC
CCCAAGGAGGCCAGAACAGCAGGCAAGTAGTTAAATTCAAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCATGTGGGAATTGATCTATATCTACTTCCAGGG
ACCATTGCCCCCTCCAAATCCCTCAGGCCAGACTGACTGGAGCAGGATGGCCACCCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAATTGAGAATTCCCC
CTGAGGCCAGTCTGTCATGGATGCTGCTGAGAATAACTTGTCTGTCCTGGGTGTCACCTGC
TTCCATCTCCAGGCCAACAGCCCTCTGCCACCTCAGCTGCCCATGGATTGGGCCT
CCCAAGGCCCCCACCTTATGTCACACTGCACTTCTGTTCAAAATCAGGAAAAGAAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATACTTGCTGTGGAAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGGACTTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAATTATTTATGATGTAGAAGTGGAGTTGTTG
TTTGATATTAAAATGGAGTTGTTG

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDMDPFGLVVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCCAGAAGTTCAAGGGCCCCCGGCCCTCGCTCCTGCCGCCGGGACCCCTGACCTCTCA
GAGCAGCGGCTGCCGCCGGAAGATGGCAGGAGGACCGCCACCGCTCCTCTGCTG
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCTATGGGTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGTATTAGCTGCAAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGGAAAGAAACTGGTGGAGGTGCTCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCG
GATCAAAATGTGACAAGAAGTGTGAGCTGGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAACCTGGAAAGGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCTCTTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAGA
CAAAGAAGGGAAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAAATGAATAACAAAAGTGGAACT
CTGCAATTAAACTGTTCCAACGGACACTGGAGAATATTCTGTGAAGCCCGAATT
TGTTGGATATCGCAGGTGCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGTAGTGTGGCCTTAGTGATTCGGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAGGCTACTTTCAAAGAAACCTCCTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGGAAATGTCAGTGGCTCACGCCGTAAATCCAGCACTTGGAGG
CCGGCGGGGGGATCAGGAGTCAGGAGTTCTAGACCAGTCTGGCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATAGCTGGCATGGTGCATGTGCCTGAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAAACCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLRLVVALGYHKAYGFSAPKDDQQVTAVEYQEAILACKTPKKT
WKKLGRSVSFVYYQQTTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARNNSVGYRRCPGKRMQVDDLNI
SIIAAVVVA
LVISVCGLGV CYAQRKG YFSKETSFQKSNSSKATTMSENVQWLTPVIPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATGGGAGGTGGCTAGCACTGAACTGCTTTCAAGACGAGGAAGAGGGAGAAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCACAGCCGGACCCCTGCAT
CATGCTGCTATTCTCGCAAATACTGAAAGACATGGGATTAAATATTACTTCTAAATAA
ATGAAATTACTAACATCTCTTGACCATCTTACATACTCCACCTTCAAAAGTACATCA
TTATATCATTAAAGGAATAGTAAACCTTCTCTCTCAAATGACATTGGGACTATGGCATT
CAATTGTGGCACTGGCACTTATTCACTGAAAGAAAACCTTGTGGTCTATGGCATT
TTGACAAATGCAAGCATTCTCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG
TGGAAATCCTTAAGGGGCCATTACATCTCTGAAGAAGAAAGCTAACAGATGAAAGGACATGCCACT
CCGAATTCACTGCTACTTGGCTTAGCTACACTAACAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGAAATCAGGCCATTGGTTACACCCAGATCATT
ATGGAAGCATTACAGTGGATTGAAATGATTTAGCTCTTAACTTCCCAGCCAGTGGC
AGCTAACACACAGATTCTCTCAGACAACTATGCAAAAATTGAAATCTCCACAG
ACTTCCAGTAACACCTACTGGCTGGATTATCTCAAACAAATTATCTCAGTCACCAAT
ATTAATGAAAAAAAGATGCCAGCTCAGCTCTTCTGTGTACCTAGAGGAAACAAACTACTGA
ACTGCCCTGAAATAGTCTCGCAACTGCAACTTACAAAGAACTTACATATTACAAACT
TGCTTCTCACATTCTCAGGAGCTTATGGCCATCAAAATCTTCTTGACTTCATCTC
AATTCAAATAGATTGCAAGTGTAAACAGTAAGTGGTTGATGCTCTCAAATCTAGAGAT
TCTGTGATTGGGAAATCCAATTATCAGAATCAAAGACATGAACTTAAAGCCTCTTATCA
ATCTCGCAGCTGGTTATGCTGTATAACCTCACAGAAATACCAGATAACGCCATTGGT
GGACTGGAAAACCTTAGAAAGCATCTCTTACAGAACAGCTTATTAAAGTACCCCATGT
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAACCTTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTGGGGATAAATAATGCT
GAGCTGATTCTTCATCGATAGTCTTGTGGATAACCTGCGAGATTAAAGAAAATAGAAGC
TACTAACACCTAGATTGCTTACATTCAACCCAACTGCACTTTTCAAGACTCCCCAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGGCTGTACCATGGTACATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATCACAGAACCCATCAGGTGTGACTGTGATCGCTG
GATGACACATGAAACAAAACCAATTGATCATGGAGCCGAGATTCACTTTGCTGGGAC
CACCTGAATTCAAGGTCAAGATGTCGGAAGTCATTCAGGGACATGATGGAATTG
CTCCCTTCTTAATGCTCTGGAGCTTCTCTTCAATCTAAATGTAAGAACGCTGGGAGCTATGT
TTCTCTTCTACTGTAGAGCTACTGCAAGAACACAGCCTGAAATCTACTGTTGATAACCTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTCTATGTCCTATCTGAGGGAAACACTA
GATATAATGCGTAACCTCCAAAGGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCCTGACTTGAAGTCTGTATGATCAAAGTGGATGATCTTTCCAAAGATAACATG
GCTCTTGTAAATTTAAATAAGAGATATTCAAGGCAATTCAAGTTTGTGCTGAAAGCA
AGTCTAAATCTCAATCTAGTGTAAATGGACAGCCCTTGTCAAGACTGAAAATCTCA
TGTGCGCAAAAGTGTGCTGAATACATCTGATGTCAAGGTATATAATCTACTCATCTGAATC
CATCAACTGACTTAAATAATTGTATTGATATTCCCTCAGATCAGAAAACAGAAAAAA
TGTGTAATGTCACCACCAAGGTTGACCCCTGATCAAAAGAGTATGAAAAGATAATAC
CACAACACTTATGGCTGTCTGGAGGCCCTCTGGGATTATGGGTGTATGCTTATCA
GCTGCCCTCTCCAGAAAATGAACGTGTGATGGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGTATTAGGTGAGCTTATCCTCTGTGATAAAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGCTCT
AAAACACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNIAKIEYSTDFPVNLTGDLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNSLQELYINHNLSTISPGAFIGLHNLLRLHILNSNRQLQMINSKWFDA
LNPNEILMIGENPIIRIKDMNFKPILINLRSLVAGINLTEIPDNAVLGLENLESISFYDNRL
IKVPHVALQKVNVNLKFDDNKNPINRIRRGDFSNMLHLKELGINNNPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFRFLPKLESMLNSALSAHYGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEEPDSLFCVDPPEFGQGNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQEIIYWITPSGQKLLPNTLTDKFVHSEGTLIDINGVTPKEGGLYTC
IATNLVGDALKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSVDKVYNLTHLNPFSTEYKICIDIPTIYQKNRKKCVNVTTKGHLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCTGGACTGGCGAAGGTGCCAAGCAAGGAAAGAAAATGAAGAGACACATGTGTTAG
CTGCAGCTTTGAAACACGCAAGAAGGAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTCCCTCTCCATGTGTCTCTCTACAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCTAAGGGCTGTCTTGTCTCTGGG
GGTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAATACCTAGAGATCTCTCTGA
AACAGTCTTACTGTATCTGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCCTCAAAAGGAGTAGCTGAAACCTTGCGACTCTGGACTTGTCCGACAATGGATTCAAAG
TGTGCAAAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCAACAACCCCTGGC
ACTGCGACTGTAACAGCAAGTCTGAGGAGCATGGCGTCAAATCATGAGACAGCCCAC
AACGTGATCTGAAACGTCCGTGGATGAACATGCTGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTGAAATCCCTGCCAAGCAGGAGAAGAAAGCAGATGA
ACCTGATGATATTGCACTGTGGTATAGTGTCCAAACTGACTGTATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCACTGAGTAAATAAGTGGTTACTCTCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACCTTAAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTAAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCACTCTCACTATTAAATGAAATTATTTTTT
AATTTAAAGCAAATAAAAGCTTAACCTTGAAACCATGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLSSGGLNVTCSANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVNL SKNGIEFIDEHAFKGVAETLQTLDSLDR
IQSVHKNAFNKLARARIANPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

TOP: 1-326 50000

FIGURE 29

ACCGAGCCGAGCGGCCGAAGGCAGCAGATGCAAGGTGAGCAAGAGGATGCTGGCGGGG
GGCAGTGGAGGAGCATGCCAGCCCCCTCTGGCTGCTGGCAGCCCACCTCTGCTGGTGC
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCAGCTGCCAGTGTGCTGCCAGG
ACCGCGCTGTGCTGCCCCGAGTGTGCTGCCAGTGTGCTGCCAGTCCCAGG
ACCGCGCTGTGCTGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGGCCTGGAGGCCAG
CTTCAACAACCTCTCAACCTCCGGACGCTGGGCTCCGCAGCAACCGCTGAAGCTCATC
CCGCTAGGCGCTTCACCTGGCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTGTTCTGGAGGACTACATGGAGGTTGGC
ACAATGACCTCGTCTACATCTCACCGGCCCTCAGGGCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACGGAGGGCTGTCCACCTGCAACGGCT
CATCGTCTCGAGGCTCGGCCACCTCAACATCAATGCCATCCGGGACTACTCCTTAAGAGGC
TGTCAGCAGTCAGGCTCTGGAGATCTCCACCTGGGCTCATCTGGACACCATGACACCCAA
TGCCCTACGGCTCAACCTGACGTCCCTGTCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCCTCCGGCACCTAGTCTATCTCCGCTTCATCACACCTCTTACAACCCATCA
GCACATTGAGGGCTCATGGTGTGAGCTGGAGGAGATCCAGCTGGTGGCC
GGCAGCTGGCGTGGTGGAGCCCTATGCCTTCGGCCCTCAACTACCTGCGCTGCTCAA
TGTCTCTGGCAACAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCACCCGCTGGCTGCGACTGTGGCTCTGTGGTGTCCGG
CGCCGCTGGGGCTCAACTTCAACCCGAGCAGCCCCAGTGGCCACCCGGAGTTGTCCA
GGCAAGGAGTCAAGGACTCCCTGATGTGACTGCCAACACTACTTCACCTGCCCGCG
CCGGCATCCGGGACCGAAGGCCAACAGCTGGTGTGGAGGGCACACAGGTGAGT
GTGTCGGCCGGGCGATGGCAGGCCCGCCGCCATCTCTGGCTCTCACCCCGAACGACCT
GGTCTCAGGCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACCTACTGTGCGACTGTGGCCGAGCTGGCCCATCAGCCAACAA
TCCATGCCCGCCACCTGCGACTGTGCGCAGCTACTCGCCGACTGTGGCCCATCAGCCAACAA
GACCTTCGCTTCACTTCAACAGCCGGGAGGGAGGCAACAGCACCCGCCACTG
TGCTTTCCCTCGACATCAAGACCTCATCATGCCACCAACATGGCTCATCTTT
CTGGCGTGTCTCTCTGCTGGTGTGCTGTGTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTGGCACGCGAGCATCAGCTCGCCG
ACGCGCCCCGCAAGTTCACATGAAGATGATAATGAGGCGGGGGGGGGGGGGAGGGACCCCG
GGGGCCGGGCAAGGGAGGGGCTGGTCGCCACCTGCTACTCTCAGTCTTCCACCTC
CTCCCTACCCCTACACAGCTCTTCTCCCTCCGCTCCGTCCCCGCTGCCACCCCG
CCAGCCCTCACCACTGCCCTCTTACAGGACCTCAGAAGGCCAGACCTGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGAGCACCGACACGCCAGAGTCA
ATAATTCAATAAAAAAGTACGAACCTTCTCTGAACTTGGGTTCAATAATTATGATT
TATGAAAATGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDGKNRICKTLNQDEFASFPHEELELNEIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPEALSHLHGLIVRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCYLGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMILHEL
LRLQBIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTLEESVFHSVGNLETLILDNSNPLA
CDCRLLWVFRRLWRLNFNRRQQPTCATPEFVGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPAILWLSPRKHLVSAKSNGRLLTVFPDGTLLEVRYAQVQDNCTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHOPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCCACCGCGTCGCACTCGGCCCGGGCTCCGAAGCGGCTGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCATCCCCAGCCCCGGGATTCAAGGCTCGCCAGCAGCCAGCC
AGGGAGCCGGCGGGAAAGCGCGATGGGGCCCCAGCGCCCTCGCTCTGCTCCTGCCTGC
TGTTCGCCTGCTGGCGCCCGCGGGCCAACCTCTCCCAGGACGGACAGCCAGCCCTGG
ACATCTGATGAAAAGCTGGTGGCTGGCACCGTGGTCTCAAGTGCCAAGTGAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCGACAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTG
GCGAACTGCCAAGTCCCTGTCACTGTCTAGGAATTCCACAGAACGCCATCATCTGGTT
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCTAACCTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGCTCACCTGGAGAAAGGGTGACCAAGAACACTCCACGGAGAACCAACCCGAT
ACAGGAAGATCCAATGGTAAACCTTCACTGTCTAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGCGAGCATCGTGTCTGTGAACCCTGAATCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCTCTGTAGGGCCAGAAGCTGTGCTACACTGTGAGGGTGCAGCAATCCAGTCC
CCCGCAGTACCTATGGGAGAAGGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAAG
CAAACATGGGCAGTACAAGGCCTACTACACCCCTAACATTGAAATGACCCAGTCCGGTGCCT
CTCTCCAGCACCTACCACGCCATCATCGTGGATCGTGGTTCTATTGTCTTCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGAGCATGCTCCAGCAGCGGACACGGCCATCATCAATGAGAGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTTAGAGGCGCTGCCACTCTG
GCCCCCAAGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCGGACTTGTACAGAGCAA
CCGCAGGGCGCCCTCCGCTTGCTCCAGCCACCCACCCCGTGTACAGAATGCTGC
TTGGGTGCGTTTGACTGGTTGGATGGGAGGGAGGAGGGGGGGGGGGGGGGGGGGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAAACATCC
CAAATCAAATCTGCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAAGAAAAGCAAAAACA
AACAAAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APADADTAIIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGTTAGGGAGGAAGGAATTCACCCCCACCCCCAACCTTCTCCTTCTCGG
CTCGGACATTGAGCACTAAATGAACCTGAATTGTCTGCGCAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGATGAATTGCTCGCTTAAAATGCTGCTTGAACTTCTGTT
GCTGGAGACGCTCTTTGCTGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAAGAAGGGGACCTACAGTAGACTGTGAAAAAAAGGCTTCACA
AGTCTGCAGCGTTCACTGCCGACTTCCAGTTTACCATTTATTCGATGCCAATT
CCTCACTCGACTTTCCCTAATGAGTTCGTAACCTTATAATGCGGTAGTTGACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGACATCAACAAACAAGAATCGTCTTCTGAAAGCAGACTTTCTGGGGCTGACGA
TCTGGAATATCTCAGGCTGATTAAATTACAGGATATAGACCCGGGGCTTCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTCGATCACCACCTGCCACCTCCGACGGTAAACAGCTGAAAACCGCTGCC
CTATGAGGAGGCTTGGAGCAAATCTCGTGTATTGCGGAGATCTGCTAGAGGATAACCCCT
GGGACTGCACTGTGATCTGCTCTCCGTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGGCAGTGGCTGCGAACGCCACCCAGACTGCAGGGTAAAGACCTAATGAAAC
CACCGAACAGGACTTGTCTTGGAAAACAGACTGGATTCTAGTCTCCGGCCCTCTG
CCAAGAAGAGAACCTTGTCTGACCCCTGCCAACCTTCAAGACAATGGCAAGAG
GATCATGCCAACACAGGGCTGCTGCCAACCGAGGTACAAAGATCCCAGGCAACTGGCAGAT
AAAATCAGAACACAGGGCTGCGATGCCAACCGAGGTACGGAAACAAACCCCTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCGAGTGCAGCACATCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAAGCCCAAGCTCTAACGTGAGGA
GCTTTTCTCAGAGATAACAGACATGCCAACCTGGGATTCTAGTCTCCGGCCCTCTG
ACCTCATTCTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACATTCAAG
AACCTTTGCACTCAGGTGGCTATACTGATGAGCAATTACTGGCACCGCTGTCCGGGA
GAAATTGCGGGGCTGCAAACCTAGAGTACCTGAAACGTGGAGTACAAGCTATCCAGCTCA
TCCCTCCGGGACTTCAATGCCATGCCAACACTGGGATCTCATTCTCAACAAACACTG
CTGAGGTCCCTGGCTGGACCTGCTGGGTCTGCCCTCTAACACTGCGCTGCCAACAA
CAATTACTCATGTACCTCCGGTGCAGGGTGCTGGACAGTTAACCTCATCCAGA
TAGACCTCCAGGAAACCTGGGAGTGTCTCCGCACATTGTGCTTCAAGCAGTGGGA
GAACGCTTGGGCTCGGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCT
TAGAAAGGATTCTATGCTCTCTCAATGAGGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACTGTTAACCTCCGACAGTAAAACAGCACTGGGTTGGGGAGACGGGACGCACTCC
AACTCTTACCTAGACACAGCAGGGTGCATCTGGGTGTTGGTCCGGGACTCTGCTGGT
GTTTGTCACTCCGCCCTCACCGTGTGGCATGCTGTGTTATCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACCTCCCGCTCCGAGATAATTCCCTACAGACAGTCTGT
GACTCTTCACTGGCACAAATGGGCTTACAACCCAGATGGGGCCCAACAGAGTGTATGACTG
TGCGCTCACTCGCTCTAGACTAAAGCCCCAACCTAGGGGAGGGCAGAGGGAGGGC
ATACATCTTCCCAACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCGCG
CCATCAGCTGGATGGCATAACTGAGATAAAACTGTGAGCTGCACACCGAACGGCCT
GACCCCTTACTAGCTCCCTCCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCTCTTGTGAGAGCCCTTGTGACAGAACGCCAGCACGACCCCTGCTGGAG
AACTGACAGTGGCCCTGCGCCCTCGGCCCCGGGGCTGTGGGGTGGATGCCACGGTCTATAC
ATATATACATATACACATATAGAGAGATAGATATCTATTTCCTGTGGATTAG
CCCCGTGATGGCTCCCTGGCTACGAGGGATGGGAGTTGACAGAAGGATGAATGTAT
TGAAATAAGTAACCTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTDVCKEKICSCNEIEGDLHVDCCEKKGFTSLQRFTA
LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPGAFGLQLVKRLHINNNIKSFRKQ
TFLGLDDLEYIQLADFNLLRDIDPGAFQDLNKEVLILINDNLSTLPANVFQYVPITHLDLRG
NRKLTKLTPYEEVLEQIPGTABILLEDNPWDCTC DLLSKEWLENIPKNALIGRVVCEAPTRLQ
GKDNLNETTEQDLCPLKNRVDSSLPAPPAQEEFTFAPGPLPTFFKTNGQEDHATPGSAFNGGT
IPGNWQIKIRPTAAIATGSSRNKPPLANSLPCPGCCSDHI PGSGLKMCNNRNVSSLADLKP
KLSNVQELFLRDNKIHISRKSHFVDYKNLILLDLGNNNIAVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAQGLQNLEYLNVEYNALQILPAGTFNAMPKLRILILNNNLRLSLPVDFAGVSL
SKSLHNMYFMYLPPVAGVLQDQLTSIIQIDLHGPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFRRKDFMLLSNDEICPQLYARISP TLTSHKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLL VFVTSRAFTVVGMLV FILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

ATGTCGACTGGCTCCCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCAACGGGCCTGGCACGGCTCCGACACATTCTCTGTGCGGCCCTAAGGGAAACTGTTGGC
CGCTGGGCCGCCGGGGGATCTTGGCAGTTGGGGGCTCGTCGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAAACGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGGCTCTCGAGCGGGACAGATCCAAGTGGAGCAGCTCTGCGTCCGGGGCTCAG
AGAATGAGGCCGGCGTTCGCCCTGTGCCCTCTGGCAGGGCTCTGGCCGGGCCCTCAG
CGGCGAACACCCCCTGCGAACCGTGTGGCTGTCGGCCCTCGGGGCTGCTACAGCCTGC
ACCAACGCTACCATGAAGCGCAGGGCGCAGGGGGCTCAGCTGGCGAGGTGGGGCGCTC
ACGACCGTGGTGGCGGCCAGSTGCGCCTGTCGCGCTCCCTGCGGGCAGGGCAGG
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGTGTGCACTGGAGCCAGGGCTTCCACT
GACCCCTGGAGAACGAGCTTGTGGGGTTCTCTCTGGCTGTCCTCCGACCCCGCGGTCTC
GAAAGGCAGACAGCTGCGAGTGGGGAGGGAGCCCCAACGCTCTGACCCGGCGAGATGCG
GTTACTCCAGGGCACCGGGTGGGGTGCAGGCCAGGCTGGAGAGATGCGATGCCACCTGC
GCGCCAAACGGTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGTCTGGCCGCGCCCGGG
GCCGGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGACAGGGCCGCTCTGGACCTTCA
TCCACCTGGGACCGAGGGTAGGTGCGCTCTGGGGGAGACAGCTCCGATCTCAGTTACTGCA
TCGGCGACGAATCGCGCTCGTGGACAACACTCTGGGGATGTTGTGTCCTGGCC
GGAGGGTACCTCCGTGCTGCAAATGCGCAGAGCTCCCTAAGCTGCTAGACGACTTGGGAGG
CTTGGCCTGCGAATGTGCTACGGGCTTCAGCTGGGGAGAGCAGGCCGCTCTGTGTGACCA
GTGGGGAAAGGACACGGGACCCCTGGGGGAGCGGGGTGCCCCACAGGGCCCGCCGGCACT
GCAACCAGCCCCGTGCGCAGAGAACATGGCAATCAGGGTGTGACGAGAACAGCTGGGAGAGAC
ACCAACTTGCTCTGAAACAAGACAATTCTAGTAACATCTTCTGGAGATTCCCTGAGATGGGAT
CACAGAGCACAGTGTACCTCCCTAAATGTCTGGGCAAGCTAACAGGCCACTATCACC
CCATCAGGGAGCGTGTATTCAGGTTAACTTACGACTCCCTCTGCCACTCCCTAGGCTT
CGACTCCCTCTGCGCTGGTCTCATATTGTGAGCACAGCAGTAGTGTGTTGGTGTATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTGCTTCAAGGAAAGCCCTCTTCCAGCCA
AGGAAGGAGCTATGGGGCCGCCGGCTGGAGAGTGTGATCTGAGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAGAGTGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGTGGCGAGTCCCTCTGGCTCTAGTGATGCA**TAGGGAAAACAGGGGA**
CATGGGCACTCTGTGAACAGTTTCACTTTTGATGAAACGGGGAAACCAAGAGGAACCTAC
TTGTGTAACCTGACAATTCTGCGAAGAAATCCCCCTCTCTAAATTCTCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCTTCCCTGATGATAAGGAGAAGTGGAGGTGCTTGTAGGA
TGGTGTGAACTGGGGGACGGGCTAGTGCTGGGGAGAGATAATTCTTATGTTTATTGGAGA
TTGGAGAAAGTGTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGAAAGGAAATGTTCTATGTTGTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCAGGGAAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGGGSKDLLFWALEERRSHCTLENEPLRGFSWLSSDPGGL
SDTQLQWVEEPQRSCTARRCAVLQATGGVPEAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFACECATGFELKGKDGRSCVTSGEGQPTLGGTGVPTRPPATA
TSPFPVQRTWPIRVDEKLGETPLVPEQDNSTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTSSATPQAFDSSSAVVFI FVSTAVVVLVILMTVGLVKLCFHESPSSQPR
KESEMGPPGLESDEPAALGSSSAHCTNNNGKVGDCLRRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTCAAGCATGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCTTTAAAGTGCCCTCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCGCCCGCGCGCGTGCAGCGTGAAGAGGGAGCGCGCGGGCAGCCGA
GCCCGGGTGTGAGCCAGCGCTGCGCAGTGTGAGCGGGGTGTGAGCGCGGTGGTGCAGGA
GGGGCGCGAACGCCCTGGCGCCACTCTGCGCTGCGCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTCACATGTGTCAGTGTGCAATTCTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGAGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTCCCCGAAGGAAAAGTAGTCCTCTCAATTTCGATTATAGACCTCGAGAGTGACAAC
CTGTGCCGTATGACTTGTGGATGTGTACAATGCCATGCCAATGCCAGCGCATGGCC
CTTCTGTGGCATTTCCGCCCTGGACCCCTGTGTCAGTGGCAACAAAGATGTGTCAGA
TGATTCTGTGCAACACAGTCGCAATGCCATGTTCTCCGCTGTGAAACCA
AACCAAAGAGGGATCAGTATTGAGGACTCTTGACAGACCTCCGGCTCTTTAAAC
CCCCAACTGGCAGACGGGATTACCCCTGCAAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAAATCAGCTTATAGAATTAAAGTGTGAGAAGTTGTGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAACTAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCACCTCGCCAATTGTGTCAGGAGAAATGAACCTTATTCAGT
TTTATCAGACTTAAGTTAATCTGAGATGGTTTATTGGTCACTACATATTGCCAAAAA
AAACTGCCCTACAACAGACAGCTGCAACACCACATCCCTGTAACCACGGGTTAA
ACCCACCGTGGCTTGTCAACAAAAGTAGCTAGACGGACGGGACTCTGGAGGGCAATTATT
GTCAAGTGACTTGTATTAGCCGGACTGTTATCACAAACCATCACTCGCGATGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTAACAGAGGGAAATTGGCAGATTCAAGCGGG
CAAGAACATGAGTGCAGGCTGACTGCTGCTGCAAGCAGTGCCCTCTCCAGAAGAGGTCT
TAAATTACATTATTGGGCCAGTAGGTGAGATGGGAGGGAAACATGCCAAACAGC
TTTATCATGATGTTCAAGACAAGAACATGAGCTCCCTGGATGCCCTTAAAGAATGCAATG
TAACAGTGAACTGTGTCATTAAGCTGATTCTGCCATTGGCTTTGAAAGAGTCTATGTTCT
TCTCAGTAGAAAAAAACTATATAAAATTACATATTCTGAAAGAGGATTCCGAAAGAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCGAGAGATGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCGGACTTATGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGCTGACAGCTGGAGCGTTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGAGATGTCAAAAAAAAGATTTAGAAGTGCATATTATAGT
GTATTGTTGTTCACCTTCAGGCCATTGGCTGAGGTGTACAATCTGCTTGCCTTCT
AATCAATGCTTAAATAAAATTTTAAAGGAAAAAA

FIGURE 3B

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYPAVGVTCVWHIV
APKNQQLIELKFKEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSSLTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLDAKKNQG

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACCGTGGCGGCCACGGCGCCCGGGCTGGGCCTCGCTTCTT
CCTTCTCGTGGCCTACGAGGTCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCAGCTGTCTGGGCCTCAGCCTTCTCAACCTCCAGGACCTATCTGG
CTCCAGGCCCTCCACCTCCCAGTCTCTCCCCGCGCTAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGTGAGCAAGTCAGACTTGAGTGTGCCACCGCCTGCTGGAGCT
GAGTGGAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAAACAGAGAGGCCCTGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAACGCCCTACGGGGTGAGGCCCTGCGG
AGTGTGGCCTTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGACCCA
ACTGTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCTATGAGTGCAGACTGTGCCAAG
GCCTGCCCTAGGCTGCATGGGGCAGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGGGGCTTCAAGGTGTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAACCCAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGAGGAGCAGATCCCAGAGTCAGCAGGCCCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGAGCAGATGTTGGCATCATCTGTGCACTGGCCA
CCCTGGCTGCTAAGGGCGACTTGGTGTACCGCCATCTCATTGGGCTGTGGGCCATG
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTCATCAAGGGAGATA
ATCGCGGCCACCACCTGTAGGACCTCTCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCTACCTG
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTTAAAAGTAGC
CCTGAAGGTGAGACCATGAGCTCTCCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGGCCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGGLVPAVLWGLSLFLNLPGPPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSELVESNWFHKQ
QEAPDLFQWLCSDSLKLCAGTFCGPSCLPAGTCGGTERPCGGYQQCEGEGTRGGSGHDCQAG
YGGEACGQCGLGYFEAERNASHLVCSCAFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCNTTEGGYRCICAEGYKQMEGICVKEQIIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLRSRDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

TOPP73 - SC650660

FIGURE 41

TGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCAGCTGGTGTGCCCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCCTGGCAGGCCCTGCGGAGCTGAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTATCCCCACCCAGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGAGCCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGTGCAGGCCGTGTCGGCTTCCAGG
AGCCGGTCCCCAAGGCCCGCTGCACAGGCACGGCGGTGTCAGGCCGCAGGCCGGGCC
CGGGTACCGTCAGGTGGCTCGCGTCCCGCAGACGGCTCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCCGTCCACGAGAGCGCTGGAAGGCCCTGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCCTGCTGACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCGCTGGCGTCCGGCAGCCACAAGCTGGCTTGCCTCGCAGGGGC
GCCAGCCGGCTGGGAGCCCCAGCTGGAGCTGCACACCTGGACCTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCGCTGTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACCTGGTGTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCCCGCAGCCCCGGAGGCCCTGGCTTCAAGTGGC
CGTTCTGGGCCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAAGGCCAGGTGGTCAGGCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCCTGGATGGCGCTCGCCAAGGAGGCTCAGCCATGGCGCCTAGTG
TAGCCATCGAGGGACTTGAATTGTGTGTTCTGAAGTGTGAGGGTACCGAGAGCTG
GGCATGACTGAACCTGCTGATGGACAAATGCTGTGCTCTAGTGACGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTTCTCAGGAATGAGAATCTTGCCACTGGA
GAGCCCTTGCTCAGTTCTTCTATTCTTATTCACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCAATTGTTACTTGTCTGTAC
TGGATCTGGCTAAAGTCTCCACCAACTCTGGACCTAACAGCTGGGTTAAGTGTGGGT
TGTGCATCCCCATCCAGATAATAAGACTTTGTAAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSRSPSARARVTVEWLVRDDGSNRRTSLIDSRLVSVHESGWKAFFDVT
WQQLSRPRQPLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPEQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

TOPAZ-2000

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGCCCTTCATATTGGCGATCTGTTGTGTCCTCG
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAAATACTCT
GTGAAGTTGCTCTGCTACTCGGGCTTTCTCCCCGTGAGGATGGAAGTTGACCA
AGGAGACACCACCAAGACTCGTTGTATAATAACAAGATCACAGCTCCTATGAGGACCGG
TGACCTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATGGTCTGAGGAAGGGCGAACAGCTATGGGAGGTCAAGGTCAAGGTCAAGTCATCGT
GCTTGTGCCCATCCAAGCTTACAGTTAACATCCCCTCTGCCACATTGGGACCGGG
CACTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAGAT
GGGATAGTGTGCTACGAATCCAAAAGCACCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACACAGGAGAGCTGGCTTTGATCCCCCTGTCAGCCTCTGATACTGGAGATA
GCTGTGAGGACCGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGATGGAAGCT
GTGGAGCGGAATGTGGGGTATCGTGGCAGCGTCCCTGTAACCCGTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGGCTATAGCGCAGGCACTTGTACAGAACAAAGAAAGGG
CTTCGAGTAAGAAGGTATTACAGCCAGCTAGTGGCCAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCTATCATCTGCAATTGCCCTACT
CAGGTGTCACCGGACTCTGGCCCTGATGTCTGAGTTACAGGATGCCATTGTCTTC
TACACCCCAACAGGGCCCCCTACTTCTCGATGTGTTTAATAATGTCAGCTATGTCCCC
ATCCTCTTCATGCCCTCCCTCCCTTCTACACTGCTGAGTGGCCTGGAACATTGTTAAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGGTGCAGGAATCTGCACTCACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTAGAGCGGGAAATTAGAGGCTAGAGCGGCTGAAATGGTTTTGG
TGATGACACTGGGTCTTCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTCTGTTGAGGAGGCTAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTAAACACCGCTGCTCAAAGAAAAGAAAACGGAGCTGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTGGGATCACGCTGACCA
ACATGGAGAACCCACTGGAAAATACAAAGTTAGCCAGGCTGGTGGTGCATGCCGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLCLFILAIIICSLALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTMCVSEEGGNNSYGEVKV
KLIVLVPPSKPTVNIPTSSATIGNRAVLTCSEQDGSPPESEYTFWKDGIVMPTNPKSTRAFSNS
SYVLPNTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGIVIAAVLVTLLI
LLGILVLFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

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Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158, 193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGCGGTTGGATGGCGCAGGGTGG
GCGTGGCGAACAGGGGCTGGGCCTGGCGCTGCTGCTGCTGGCTCGGACTAGGCC
GGAGGCCGCGAGCCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCG
GCTCGTGCACCACCAAGTCCAGTCCGCACCAGTGGCTATGCGTCCCCCTACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGAGGCC
ATGTACCCGAAAGGGCAATGCCACCCCTGGCTCCCTGCCCTGCAAGGGCGTCA
GTGACTGCTGGGGAACTGACAAGAACTGCGCAACTGCAGGCCCTGGCTGCCCTAGCA
GGCGAGCTCCGTTGGCACCGCTGAGCGATGACTGCATTCACTCACGTGGCGTGCAGGCCA
CCCAGACTGCCCCACTCAGCGAGCTGGCTTGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCACTCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCCTGTGCGGAATGCCACATCCTC
CTCTGCGGAGACCACTGGAAGGCCAACTGCCATTGGGTTATTGCACTGCTGCCGTG
TCAGTGAAGCCTGGTACCGCCACCCCTCCCTTTGTCCTGGCTCGAGGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCATGAAGGGACTCCCTGCTGTCAAAACAGAAC
CTCGTGCCTTGAGGACAAGCACTTGCCACCAACCGTCACTCAGCCCTGGCGTAGCCGACA
GGAGGAGAGCAGTGTGGATGGTACCCGGCACACCAGGCCCTCAGAGACCTGAGTTCTT
CTGGCACGTGGAACCTCGAACCCGAGCTCCCTGCAAGAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCGAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGCTGAGGGTGGCGATTAAAGTGTCTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCTQKGQCPPPGLPCCPTGVSDCSGGTDKKL
RNCsRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPVGNAATSSSAGDQSGSPTAYGVIAAAAVLSASLVATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCCACGGTCCGGTCTCGCTCGCTCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAAGGAGGAGCTGCATGCATGAGACCCACAGA
CTCTTGAAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCAGACAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTTAGCTGGCGTGTGCTCGGCCCTGCACAGCTCACGGGGGGTT
CGATGACCTTCAGTGTGTGCTGACCCCGGATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTCTTGAAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAAGAGACTGTGTTGAAGCATTAAATGAAACCCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAACGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGG
TACCCCGACCTACACATATGGTTCTATTAGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAGGCTGCTGAGACCTCTAGCCCTTCTAATGGCTATGTAACATCTGAGC
TCCAGACCTCCCTCCGGTGGGACTGTGATCTCCATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CTTGCTCTGGAAGGCCAAGTCTGTCACCTCCAATGGTAGTGAGTCACGGAGATTCTGCT
GCCACCCGCGGCCCTTGAGCGTACAACCACGGAACCTGTTGAGGTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTCAAGGCCACTTCCCCCAGGGGGCCTCCCGGAG
TTCCAGCAGTGACCCCTGACTTTGTGGTGGTAGACGGCGTGCCTCATGCTCCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGTACATGGCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGGCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCCGCTTGGACAACCTGACATA
ATGCCAGCAGGCCAGGGAGGTGGCATCCACCGCCAGGATCCATGCCACTGGGT
GTTGTTCTTAAGAAACTGTATTGATTAATTTCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTCTCTTGAGTAAAGACAAATGTAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGTGATCAAGTC
CTGTTCTTGTGACACAGACTGATTAATTAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGVFFEGSVARFHQCQDFKLKGATKRLCLKFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLGDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSYKITYTCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAAEVASTSPGIHHAHWVLFLRN

SIGNAL SEQUENCE

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCCACCGCTCCGCTCCGCCTCCCCCCCCTCCCGTGC GGTCGGTCCGTGGCTAGAGA
TGCTGCTGCCCGGGTGCAGTTGTCGCGCACGCCCTGCCCGCAGCCGCTCCACGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCGAGTCGGGCCATGAGGCCGGAACCGCGTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGTGCGGGCCGACGGGTCGCCCTGCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCAGTCTGCCGGGAGGGACACAGAGGCTGTTA
TAAAGTCATTTACTTCATGATACTTCTCGAAGACTGAACATTGAGGAAGCCAAAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCAATTGAAAAACCTCTGCCATCTGATGGTGA CTTGGATTGGCTCAGGAGCGTGA
GGAGAAACAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT
ACAATTTAGAACATGGTATGTGGATGAGCCGCTCTGGCAGCGAGGCTGCGTGTT
TACCATCAGCCATCGCACCGCTGGCATCGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACATTCAATTGCAAATATTCTGATGAGAAACCAGCAGTT
CTAGAGAACGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCAT
CTTAATCCCCAGCATTCCCTCTCCTCTGGTGGTCAACCACAGTTGATGTTGGTT
GGATCTGTAGAAAAAGAAAACCGGGAGCAGCCAGACCTAGCACAAAGAACACACCATC
TGGCCCTCTCTCACAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAACGCTGACTTAGCTGAGACCGGCCAGACCTGAAGAATATTCAATTCCAGTGT
CGGGAGAACCACTCCGATGACATGCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGACAACAATGGAAAAGGAAATGATAAGC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAAACAAGCTTAGATCAGGCTCTGT
GGATGAGCATGGTCCCCACGACCTCCTGGACCCCGACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGCTGGCACATAGTA
GAGTCTCAATAATGTCACTGGTTGGTTGATCTAATTAAAGGGACAGAGCTTACCTG
GCAGTGTAAAGATGGGCTGTGGAGCTTGAAAACCACCTCTGTTTCTTGCTCTATACAG
CAGCACATATTACATACAGACAGAAAATCCAGAACATCTTCAAGGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGCAATTCTCATATGTTTTCAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRILLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPETQEEDAKKTFKESREAALNLAYILIPSIPLLLVL
VTTVVCVWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFS PDQMGRSKES
GWVNEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCCCTCAGGGCGGGAGGCACAGCGTCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTTCACTGCCTTGTCGGACCCCAGTGGCGCTCTGACCTCGTGGCTACTGCCTGCACC
AGCGCGGGGTGGCCCTGGCCGAGCTGCAGGAGGCGATGGCCAGTGTCCGGTGACCGCAGC
CTGCTGAAGTTAAAATGGTGCAGGTCTGTTCGACACGGGGCTGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCCAGCTATTAGAGGTCCCACCCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGAAAGACATTCCCTTC
TTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGGTGTGCTGGCTGGCTTTCCAGTGTAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGTCTGTATCCCAACTACCAAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAACAGAGGCCGGAGGAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAGGGACAGGATGGCATTGACAGTAGTGTATAAGTGGACTCTTCATCCTCCT
GGACAACGTGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATGCAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCTAGAGAGAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCGGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTAAATGACCCGGGATTTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACTTACAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCAGAAAATACCATGCACTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATAACATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMQVVFHRGAR
SPLKPLPLEBQEWNPNQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVMQQMFALGERLRKNYVEDIPFLSPTFPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNEYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPLCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAACTAAATATTGCTGCTTGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC GTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCGGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGTGTCAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGA
GCACCAAGAACCGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCGCAAGGTGG
TGTGCCGGCAGCTGGATGGGAGGGCTGACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAACCTTC
GGATTGCCCTCTGGGCCTGGGGAGAACACCTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGGCACTG
GAGGTGCTGACAAGGGTATGGGCTCTGCTGTGATGACAAC TGAGGAGAACAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGAAGTCCCTCTCCCTCCTCAGGACCGGA
AATGCTATGCCCTGGGTTGGCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC CAGCACAGATTGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGGACTTAACTTGGTGCCTCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAAC TACATCA
CCACCTTCTATGTCCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTTGTT
CAACTACTTAAATAACATTCTCACACACACACACACACACACACACACACACACATA
CACCATTGCTCTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACT
TTCTAGAGGAACGGATTAAAGGATAAAATTCTGAATTGTTATGGGTTCTGAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEEQKGQWGTVCDDGWDIKDVAVL
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVYDCSHDEDAGASC
ENPESSFSVPPEGVRLADGPGHCKGRVEVKHQNWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCGSRLEVHKGVWGSVCDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGTCCCGGGACCGTGGCGGACCGTGGGCCGCTACCAGGAAGAGTCTGCCAAG
GTGAAGGCCATGACTTCATCACCTCACAGGCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGCTTCGGCCCTCTCCGGCTGCTGCAGTGGTGCGCGGAAAGGCCACCTGCGGAATGCTG
TGGTGGTGTACACAGGGGCCACCTCAGGGCTGGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGTCAAACGGGTCTGTGGCCGAATGGGGCCCTAGAAAGAGCTCATCAGAGA
ACCTTACCGCTTCTCATGCCACCAAGGTGCAAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGG
TGTGGACAAGGGGTATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGACTCC
TGCCCTCCATGATCAAGAGGAGGAAGGCCACATTGTGCCATCAGCAGCATCCAGGCAAG
ATGAGCATTCCCCCTTCGATCAGCATATGCAAGCCTCCAAGCACGCAACCAGGCTTCTTGA
CTGTCTGCGTGGCGAGATGGAACAGTATGAAATTGAGGTGACCGTATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCAACCACAGGCCAGGGCGAAGGCCCTGGAGGTGGCCAGGATGTTCTTGCTCTGTGG
GAAGAAGAAGAAGATGTGATCCTGGCTGACTTACTGCCCTCTGGCTGTTTATCTCGAA
CTCTGGCTCTGGCTCTTCAGCCTCATGCCCTCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGACTCTGACCAAGGCCAGGGCAGGGCAGAGAACGACTCTTAGGTTG
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTCCAGGGTGAGGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAAACTAGAAATAAACATCTCAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCCATGGCCAACCTTGTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLGCLGVFGFLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPVLVTFDLTDGAI
VAAAEEILQCFCGYVDIL
VNAGISYRGTIMDTTVDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCCACGCGTCGGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACCAAACACGCTCGCAGCCACAAAAGGGATGAAATTCTCTGGACATCCTC
CTGCTTCTCCCCTACTGATCGTCTCGTCCCTAGAGTCCTCGTGAAAGCTTTTATCCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCAAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAAATG
GAGATGTTAGTATTAGTAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA
GGCATTCTCTCGCAATGCGAAGAATAACCATGGCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCGGTCCCCCTCTACTGGCTACTGTCAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGTACAGATGAACTGGCTGCCCTACAATAACTGGAGTCAAAACACATG
TCTGTGTCTAATTCTGAAACACTGGCTCATCAAAATCCAAGTACAAGTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGTGATGCAATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCATCTCTATAGCTTTAACACATTGGAAAGGATCCTCGAGCGTTT
CCTGGCAGTTAAACGAAAATCAGTGTAAAGTTGATGCACTTATTGGATATAAAATGA
AAGCGCAAAGCACCCTAGTTCTGAAAACACTGATTTACAGGTTAGGTTGATGTCATCTA
ATAGTGCAGAATTAAATGTTGAACTCTGTTTCTAATTATCCCATTCTTCATA
TCATTTTGAGGCTTGGCAGTCTTACATTACTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAAATACCTTAGGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGTTGCAA
ATTGTACCTAACCGTTTATTAAACATATAATTATTATTGATTCACCTAAATTGTTG
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAACTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTCACAATGAATATCATGAACCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAACATTCT
GCACAGGGAAAGCTAGAGGTGGATAACAGTGTGCAAGTAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKS
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSI
LWNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNGHIVTVASAAGHV
SVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTS
LGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCTCCGGACGGCTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTCGCCGCACCCGTAGAGA**T**GTTGGTGCATGTGGAAAGGTATTG
TTTCGCTGGTCTGTGATGCGCTGGCCCTGTGATGGCTGGCTTCTGCCTTATAACAGAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCTCACCCCTACATTGAAGC
TGGGAAGATCCAAGGAAGAGAATTGAGTTGGTGCAGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGCTTCCTCACCGTGATAAACAGACTAACACAGCAACCTCTTCGTTTC
TTCCAGCTCAGATACAGCAGAAGATGCCCTAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGGACTTTGTGAAACATGGCCCTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCAAACGCTCTCATGCTTACATTGACAATCCA
GTGGCACAGCTTCAAGTTACTGATGATAACCCACGGATATGCACTGAGTCATGAGGACGATGT
AGCACGGGATTATAACAGTCCACTAATTCAAGTTTTCCAGATATTCTGAATAAAAATA
ATGACTTTATGTCATGGGAGCTTATGCGAGGAAATATGCGCCACGGGATTGCAACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGGTTGAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGCAAGATTCTGTACCAAATTGGCT
TGTGGATGAGAAGCAAAAGACTTCCAGAACGACTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACACTGGTTGGCCCTTGAATAACTGGATAAACACTAGATGGCAGCTAAC
AACTGATCCTTCTTACTTCCAGAATCTTCAAGGATGTAATTACTATAACTTTTCGGT
GCACGGAACCTCAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTATGATGGAATATGGTGAAGACTTCCGGAGA
AGATACAGTACAGTCAGTTAGGCATGGTTAAGTGAATCATGATAATTATAAGGTTCTGA
TCTACAATGCCAAGTGGACATCATGTCGGCAGCTGCCCTGACAGAGCGCTCTTGATGGC
ATGGACTGAAAGGATCCCGAATAAGAAGGAGAAAAAAAGTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTCACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTCACCTATGACCAGCCTCTGAGAGCTTTGACATGATTATCGA
TTCATTTATGAAAGGATGGATCTTATGTTGGATA**A**ACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCTGAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTCTTATCTGCAAGATTTCATCAATAAAAATTATCTTCTGAAACAGTGAGC
TTTGTGTTGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACT**T**AAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTGGTGGCTGTAAGAGGTTAATTCTCTAAGAGTAAGTGAAGGACTTGGCATGCCGTGAGGT
TAACAAACAAAGCTGTAACATCTTCTGCAATAACAGAACAGTTGGCATGCCGTGAGGT
GTTTGGAAATATTATTGGATAAGAAATAGCTAATTATCCAAATAATGGATGAGCTATAA
TAGTTTGGGAAAAGATTCTCAAAATGTATAAAAGTCTTAAAGACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPKGDSGQPLFLTPYEAGKIQKGRELSE
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLDRDFPWTTLSMLYIDNPVGTFSTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECTEHIRKQNWFEEAFEILDKLLDGDLTSDPSYFQNVTG
CSNNYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNGQTFTNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAAATCCCAGTCTTGGGCTACAACAT
TTTCCCTTCAACAAGTCTAACAGCTTCTAACAGCTAGTGATCAGGGTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACAGCTCTT
CCTCTGTGATAACAGACATGAGAAAGTGAAGAGATGCAGCGGAGTGAAGGTATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCTAACAAAGCTTCAAAAAAAGGGAGCAGTCTTCACTGGCTGGGAT
AAAGCTGCGGTAGGATAGGGAAAGACTGGGTTAGTCTTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTAACTCTCTGGGAGTGAACAAAGCATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTTAAAAAGCAAGTATTATAGATAAAAGGCTAGA
GACCAAAATAGATAACAGGATCCCTGAACATTCTAAAGAGGGAGAAGTATGTTAAAATA
GAAAACCAAAATGAGAAGGGAGACTCACAGAGCTAACCAAGGATGGGACCCGGTC
AGGGCAGCCTTGTCTCCGGAAATTATTTGGCTGACCACTCTGGCTTGTCTT
GCAGAATCATGGAGGGCCAACCGGGAAAGGTGGAGCAGATGAGCACACACAGGAGCGCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCGCTCTGGTCTCTAGTGTCTGGCTGCTGGCCCGCCAGCAGCCGC
ATGCCCTAGTCAGCACCTTCACTCTGAGAACATCTGACTGGACCTTCACCCACTTGACCGT
CCACCAAGGGAGGGGGCGCTCATGGGGGCATCAACCGGGCTTAAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAAGACAGGGCCAGAAGAGGACAACAAAGTCTGTTACCG
CCCTCATCTGTCAGGCCCTCAGCGAAGTGTCTACCCCTCACCACAAATGTCACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGAGGCTTACAGGGGGTCTGCA
AGCTGCTGCGCTGGATGACCTTTCATCTGGTGAGGCCATCCACAAAGGAGCACTAC
CTGTCAGTGTCAACAAAGACGGCACCTGTACGGGTGATTGTGCGCTCTGAGGGTGGAGA
TGGCAAGCTTCACTGGCAGGGCTGGATGGAGCAGGATTACTTCCGGACCCCTGTCCA
GGCGGAAGCTGGCCCGAGACCTGTAGCTCTCAGGGCATGCTGACTATGAGCTACACAGGAT
TTTGTCTCCCTCTCATCAAGATCCCTCAGAACACCCCTGGCCCTGGCTCTCCACTTGTACAT
CTCTACATCTGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGGGCGAGA
CCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCTTCTACACCTCACGCATCGTCCG
CTCTGCAAGGATGACCCCAAGTCCACTCATAGTGTCCCTGGCCCTGGCTGACCCGGGC
CGGGCTGGAATACCGCCTCTGCAAGGTCTTACCTGGCCAAAGCTGGGACTCACTGGCC
AGGCTTCAATATCACCAGCGAGGAGTGTACTCTTGCCATCTCTCAAAGGGCAGAAG
CACTATCACCACCCGCCGATGACTCTGCTGTGCTTCCCTATGGGCCATCAACTT
GCAGATCAAGGAGCGCTGCACTGCTGCTACCGGGCGAGGGCAACCTGGAGCTCACTGGC
TGCTGGGGAGGAGCTGCACTGCAAGGGCCCTGTCCCATGATGATAACTCTGTGGA
CTGACATCAACAGCCCTGGGAGGCTCAACTCAGTGGAGGGCTGACCCCTGTACACCC
CAGCAGGGACCGCATGACCTCTGTTGGCTCTACGTTAACAGGCTACAGCGTGGTTTG
TGGGGACTAAAGGTGGCAAGCTGAAAAGGGTAAGAGTCTATGAGTTCAAGTGTCCAATGCC
ATTCAACCTCTCAGCAAAGACTCCCTTGGAGGTAGCTATTGGTGAGATTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAGAAGGGTTAATTGTG
ACTTAGCTCTAGCTACTCTCCAGGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCACAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLGQASLFAPPGNWFSDHSALCFAESECEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDERSVVLSSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLNNVNKLIIIDYSENRLLAGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMGYGIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFAASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDLSAQAFNITSQDDVLFAIFSKGQKQYHHPPDDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWLKGKDQCTKAPVPIDIINFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGCTGAGTGGGACTGGAGTTGGGAACCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCCGCGAGCCGCCACGGCTGGACTCTGTGCTGCTGGCTTCCTGGCTC
GCAGGGCTGACTTGAGCACCTGCTCCCTGCGCTCGGCATCGAACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTCTATGCTGGAGGATTCCACCTTGTGGATCTCGGGCTCCCATCCACTATTTCCTGTTGCCCCAGGGAGACT
GGAGGGACCGCTGCTGAAGATGAAGGCTGTGGCTGAACACCCTCACCCACTATGTTGGACCTGCTCATG
AGCGAGAAAGAGGCCAAATTGACTTCTCTGGGAACCTGAGACCTGGAGGGCTTCGCTCTGATGGCCCGAACAGATCG
GCTGTGGGTGATTCCTGGCTCAGGGCCCTACATCTGCACTGGAGATGGACCTTGTGCTC
TCCAAGACCTGGCCATGAGGCTGAGGACAACCTAACAGGGCTTCACCGAACAGCTGGACCTTATTTGACCAC
TGTGTTGGCTGTCACACTCGAGTAACAGCTGGGGGCTCATCTGGGACCTTGTGACCTG
TCTCTATAATAAAAGACCCGCATACATGGCCCTACGGCTCAAGAACAGGACTGGAGGACCTGGCATTTGGAACACTG
TCCGTGAGGAGGAACTGGGACTGGCAAGGGGATTTGCTGGGACCCATCAACTGGCTGAGT
CAACACAGAGCTGCACTGACCAACCTTCTTCACCTCAGGGACTCACGCCAAGATGTGTGAGGAT
ACTGGACGGGGTGGTTGACTCTCTGGGAACGGGGCCCTAACAAATATCTGGAACTTCTGAGGTTTTGAAACACGGTGT
CTGCAATTGTGGACCGGGCTCTCCATCAACCTCTCATGACTAACAGTCAACAGCTATGACTATGATGCTGTGCTGACAGAACGGGG
GAACCATGCACTTCCATGACTAACAGTCAAGTCAACAGCTATGACTATGATGCTGTGCTGACAGAACGGGG
ATTAACGCCAACGGGACTCTGGGACTCTGGGCTCTCCATCGAGGCACTCCCTCTCCCACCCACCTG
ACCTCTTCCCAAGATGCCCTATGAGGCTTCAACCCAGTCTGACTCTGTGCTGAGGACCTCAGTACGGGCTCAAGTAC
TGGGGAGGCCATAAGGACCTGAGAACGGGACATCGAGGAACTGGCCAGTCAATGGGGAAATGGCAAGTCT
TCGGGATCATCTTGTAGAACAGGATCATCTGGCTCTGGGACTCTGTGAGGCTGAGGCTGAGGCTGAGGCT
TCTGGTGAACACAGTATCCATAGGATTCTGGACTACAAGAACACGAGAATGCTGTGCTCCCTGATCAGGGT
ACACCCGCTGCTGGGAGATCTGGTGGAGAATCTGGGAGACTCTGGGAGACTCAACTTGGGAGGAAATTTGATGACAGGCGGCCAAG
GCTTAATTGGAAATCTCATCTGAATGATTCAACCCCTGAAAATCTCAAGATCTTACGCTGGATATGAAGAAGA
GCTTCTTCTCAGGGCTCTGGGCTGAGAACATGGGNTCTCCAGGAAACACCCACATTACCTGCTTCTCTCTCTCTCT
GTAGCTTGTGTCATCAGCTTCAACCCCTGACACCTTCTGAGCCTTCTGAGCTGGGGAGGGCTGGGAGAAGGGGTTGATTCA
TOAATGGCAGAACGACTTGGACGTACTGGAACTTGGACCCCAAGAACAGGCTTACCTCCAGGCTCTGGTTGA
GCAGGGGAACTAACAGGTCATGGTTTGAGGAGAACAGTGGCAGGGCTCATTAACAGTTACGGAAACCCCC
ACCTGGGAGAACAGTACATTAAGTGAAGCTGGGCCCCCTCTGGTGGCTGAGCTGGGGCT
CTCTGGGAGCTGAAGCTGGTGGCTGCTGGGCCACCCCTACTGCAAAGCATCTCTTAACTGAGAACCTCAGGG
ACTGGGGGACTAGCTGGGCCCCCTGCTCAGCTCAAACCCCTAACGGCTGAGGGAAAGGGGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTACAGGGCTGCTTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
AGCTAATCAGATGGCAGGCTTGGGCTTGGGAGGAGAACAGGCTGGGGCTGGGAGAAGGGGAGC
TGGGAGCATCTGACTGGACTCAGGGCTGCTTGTGAGGCTGAGGCTGGGAGGAGAACAGGCTGGGAG
TTTATCCCCGAAATCTGGGTGTCACCAAGTGTAGGGGGAGGGGTGTCACCTGAGCTGACTTTGTT
CTCTCTTCAACACTCTGTGAGCTTCTTGGATTCTGGAGAACCTGGGCTGAGAACATGTGACTTCTCTT
TCCCCTTCCCAACTCTGGCTGCTTCCCAACAGGGTGACAGGGCTGGCTGGAGAACAGAACATCTCACCTGCTCTTCC
CAAGTTAGCAGGGTGTCTCTGGTGTGAGTGGAGGACATGGCTGAGTCTGGCAGAACCCATGGCCCATGTCATCTGCA
CATCCAGGGAGGGAGGACAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACCCATGGCCCATGTCACATCCAGGG
AGGGAGGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACCCATGGCCCATGTCACATCCAGGG
GGAGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACAGGCCATGGCCCATGTCACATCCAGGG
ACAGAAGGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCAACAGCAGGGCAGAGCAGGCCCTCC
GAAGTGTGTCAGGCTGAGTCCGATTTGAGGCTTGTGAGGCCCCAGGCCAACACCTGGCTTGGCTACTGCTCTGA
GTGCACTAAAGCTATAACCTGATCACAA

FIGURE 64

MTTWSLRRR PART LGLLLL VV LGFL VL RRL DWST LVPL RL RQL GLQAK GWN FM LED ST FW
I FGG S I HY FR V PREY WR DR LL K MKAC GLN T LTT Y VP WNL H E PERG K FDF SG NLD LEAF V LMA
A EIGL LW V IL RGP Y IC SEM DL GG L P SW LL QDP GM RL RT TY KG FTE A VD LY FD HL M SR VV PL Q
Y KR GG PI IA V QV EN EY GS Y NK DPA Y MP YV KK AL ED RG I VELL LT SDN K DGL SK GIV QGV LAT
IN LQ S TH EL QLL TT F LF NV QGT QPK MV ME WT GW FD SW GG PH NILD S SEV LK TV SA IV DAG S
S IN LY MF HG GT NF GF MN G AM HF HD Y KSD V TS YD Y DAV L T EAG DY TAK YM K LR DFF G SIS GIP
L PPPP D L LP K MP Y EPL TP VLY LSL W DAL K YL GEPI K SEK P I N M E N L P V N G G N Q SFG Y I LY
T SIT S S G I L S G H V H D R G Q V F V N T V S I G F LD Y KTT KIA V P L I Q G Y T V L R I L V E N R G R V N Y G E N
I DD QR K GL I G N L Y L N D S P L K N F R I Y S L D M K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A
L Q F T E T P H I L G R N Q Y I K

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCCTGGGCTAGCTAGGTGAGGGGTGGACGGGTCAGGACCC
CTGGTGAGGGTCTCTACTTGGCCTCGGGGGTCAAGACGGCACCTACGCCAAGG
GGAGCAAAGCCGGGCTCGCCCGAGGCCCCCAGGACCTCATCCTCAATGTTGGAGGAATC
CGACACGTGACCGTCTGCGCGTCTCAGACTAGAGGAGGCTGTAAACGCC**ATGGCTCC**
AAGAACGCTGCTGGCTCTGGCTCGTGTGCTGGCAGCCTGCACTACTTCTGGGTACCGCGGGTCTTGGGCCAC
GGCACAGACACTCGGTGCGTTCTGAGTGGATAGGGGTCTAGACCGGTTTCTCTAGACGGGGCC
CGTCTCGCTATGTGCTGGCAGCCTGCACTACTTCTGGGTACCGCGGGTCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGCCCTAACCGCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATGGCTTCTGA
ATGAGGCAGCTAGGACACTGTTGTCATCTGAGACAGGACCTCATCTGTCAGAG
TGGGAGATGGGGGTCTCATCCTGGTTGCTCTGAAACCTGAAATTCTAAGAACCTC
AGATCGACTCTCCATGGCCAGTGAGCTCTGGTCAAGGTCTTGTGCTGCCAATGATATATC
CATGGCTTATCACATGGGGCAACATCATTAGCATCAGGTGGAGATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTGGCTTCCACCAAGATGGCCCTGAAGGACTCTAACGTTGGCTCCCTCCGGG
GACTCTAACCTACGTGATTTGGCCAGCTGACAACATGACCAAATCTTACCCCTGCTT
CGGAAGTATGAAACCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGGCCAGATCACTCCACACGGTCTGTCAGCTGTAAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAAACATGTCATGTTCCATGGAGGTACCAAACCTTGGATATTGG
AATGGTGCCTGATAAGAGGGAGCCTGGCTTCTGGATTACTACAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCCACACCTAACAGTTTGTCTTGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGGACCTTTACCTCCCGAGGCCAAGATGATGCTTGGACCTGTG
ACTCTGCACTGGTTGGCATTACTGAGCTTCTGAGCTTGTGCTTGGCCCGTGGGCCAT
TCATTCAATCTGCAATGACCTTGGCTGAGGCTGTCAGACGAGGACATGCCCTCATGTTGACC
GAACCTATATGACCCATACCATTTTGGCCAAACACCATCTGGGTGCAAATAATGGAGTC
CATGAGCGTGCCTATGTGATGGTGGATGGGTCTGGGTGAGGCAAAATATGAG
AGACAAACTATTGGAGGGGAAACTGGGTCCTAACACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGCTAACAGCAGTGACTTCAAGGGCTGTTGAAGCCACCAATTCTG
GGCCAAACATCTTACCCAGTGGATGATGTTCCCTCTGAAATTGATAACCTTGTGAAGTG
GTGTTTCCCCTCCAGTGGCAAAATGGCCTATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAACATTTCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCAAGTCTGGCAATGGGTTAACCTGGGCCGACTGACAAAGCAGGGCC
ACACAGACCTCTACGTGCAAGATTCTGCTGTTCTAGGGGAGCCCTAACAAAATTAA
CATGCTGAAACTAGAAGATGACCTCTCAGGCCAACGTCATTTGGATAAGCCTATC
CTCAATAGCAGTAGTACTTGTGCAAGGACACATATCAATTCCCTTCTGAGTACACTGAG
TGCCTCTGAAACCAATGGAGTAAAGTGGCA**CTGAAAGGTAGGCCGGCATGGTGCTCATGC**
CTGTAATCCAGCAGTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAGA
CCAGCCTGGCCACATGGTAAACCCGCTCCACTAAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAAATCC
AGGAGGCAGAGGTTGCACTGAGTGGAGGTGTAACACTGCACTCCAGCCTGGTGACAGTGA
GACACTCCATCTAAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLPQLSLLPQADTRSFVVDRGHDFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLHYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKGCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQGQNHSRSVSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALARDFVISKFQEVLGPLPPPSPKMML
GPVTLHLVGHLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSGFSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWNWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLVYPRFLFPRGALNKITLLEEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGCTCGAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGCA
ACCCACAATATGGCCTACATGTTGAAAAAGCTTCATCAGTACATATCATTGGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAAGGAATATT
CTTCGAAAAGTCAGAGAAAGAGAGCAGTTTAGTGACATTCCAGATGTCAAAAACGATTT
GCGTTCCCTCTCACATGGTAGACCAGTATGCCAGCTATATTCAAGCGTTGGTGTGTT
CTTGTCAAGGTTAGTGAAAATAAACTTAGGAAATTAGTTGAACCATGAGTGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACACTCACAGACCTGGATGTGCTAAAGCTTGA
AATTCCAGAAGCTAAATTCTGCTAACAGATTCTCAATGACTAACCTCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAGTTGAAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTTGGCTGAAATTCTGCCTGGGTGATTTGCTCAAAA
CCTTCGAGAGTTGACTTAATAGGAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCCGACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAGTT
CCCTCCAACATTACAGATGTGGCTCACATCTAACAAAGTTAGTCATTCAATGACGGCAC
TAAACTCTGGTACTGAAACAGCTTAAGAAAATGATGTAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAAATCCCACATGCTTTAGCTCAGCTCTCTAAATTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAATCATGAGTTCCAGCATTAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACCTTATTCTCTAACACAAAGCTCGAACCTTACAGTGGCAGTATT
AGTTTACAGAAACTCAGATGTTAGATGTGAGCTACAACAACTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCACTGAGCTTTGATATCACTGGGAAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCAATAAGTTGAGGACTTTGATCTGGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAAACTG
CTTGGACCGCCCTGCCAGGCCAGCTGGGCACTGTCGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAAGATCACCTTTGATACCCGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAATGGATTTAAACTAAGATAATATGACAGTGATGTCAGGAAC
AACTCCCTAGATTGCAAGTGCACGTACAAGTTATTCAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTCATGTTGAGGTTTAAGTCATTCAATTAACTTAAATTGTTGTAACATTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTLDVLKLELIPEAKIPIAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLHLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTLKLLVLNSLKKMMNVAELELQNCELERIPIHAIFSLSNLQELDLKS
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRLCDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMMLKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGACTTGTGATTTCATTCATTCTTTCAITGACAAACTGACTTTTTATTC
TTTTTCCATCTCTGGCCAGCTGGGATCCTAGGGCCCTGGAAAGACATTGTGTTTACACATAAAGAT
CTGTGTTGGGTTCTCTCTCCCTCCATGGCATTGGCATTGCTTACTGGTTGTGGGGAGGGAGACACAGTGG
GCTCATGCTTGCTGCACATTCTGCTTAGGTACATCGAACGTTGGACTCCATACAGTGAATATGCCGTGTC
ATCGCTGGTGTATCTGGCGGCTTGCTCCTGCTGATAGTTCTGCTGCTGCTGCTTACTTCAAAATACACAAAC
GCGCTAAAGCTGCAAGGGAAACCTGAAGCTGTGGCTGAAAAAATACACAACCCAGACAAAGGTGTGGGGCAAG
AACAGCCAGGCAAACACATTGCCACGGAGCTGTGCTGCCCTGCGAGCTGTGAAAGGATATAAGATGTGCG
AGTTTGATTCCCTGCCACCTTGTGCTGGCAGATAAATGGGGCCCTGAGGTTAGGAAGGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCATGATGTCATAGGGCCACCTGTTGTGATGTGAGGGCACAG
CTCCCATCAGTTCATGGAAAATAACTCAGTGCTGCTGGGAAACAGCTGCTGGAGATCCCTACAGAGGCTTC
CACTGGGGGAACCCCTCCAGGAAGGAGTGGGGAGAGAACCTCAGTGGGGATGCTGATAAACCAGTC
CACAGCTGCTCTATTACACAAATCTACCCCTGCTGGCAGACTGACCTTCCCTGGAGGTGTCGAAA
GCTGATGTAACACAGGCTATAAAAGCTGTGGCTTAAAGGCTGCCAAAGAGCTTGTGCAA
ATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTAAATTCTCTCTGTTGGGGAGCTGACAAATGGCGAGGCTGAAAGGAAT
GCAAGCTGCACAGTCAGCTAGGGGTGCCATATGGCAGAGGCCAANAGCCATGATCTGCAACTCAATCCC
AGTGAAGAATGCCACCTGGCAGATAAGGAGCAGAAACAAAGCATCAGAAATTATCTTCTTCTATGTCAGCT
GATCCAGATGGAAAGCTGTGAAAGTAAATTAAGGCTTCTTGTGATTCATCGGCTTCAAGTGGGCTCTGAGGG
CAAGTCTGCTGAGTAAACAGGACTGTTCTGCTTGAATGACCTGGAGTCAATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAAGAATGCTTCTTGTCTTACTACTCTCTCTCAACATCTTAACTCAATTC
GGCGGTTACCTGGATACCTGGAAAGGATCTTCACAGCCCCAATTAACCAAAGCCGATCTGAGCTGGCTTAT
TGTGTTGGACATACAGGAAAGGATTAACAGATAAAAACTCTAACCTTCAAGAGATTTTCTTCTATGTCAGCT
AAACAGTCCAATTGATTTCTCTGCTCATCTGATGGCCCTCCACCAACTCTGGCTGATTGGACAGGCTGT
GGCCGTTGACTCCACCTGGCAGATAAGCTCTGATCTGCTGTTCTACAGATTATGGCAATTCT
TACCGGGGATTCTCTGCTTCTACACTCAATTATGCAAGAAACATCAACACTACATTGCTCTCT
GACAGGATGAGATTATAAGCAGAACTCTACCTGAGGCTTTAACTCTAATGGGATAAACTTGAACAACTAAAA
GACCCAACTTGGCAGGCAAATATATCAAATGTTGTTGAAAGTATGAGCTCTGCTTCTTCTGATCTGAGCTGATC
AAGGTTAGAAGATCAGTCATTAACCTACACCAATATAATCACCTTCTGCTCATCTCAACTCTGAGCTGATC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAATGGGACATAATTCTACAGTGAGGATAATATCACAA
GAAGATGATGTAATCAAAAGTCAAAATGCACTGGGCAAATATAACACCCAGCATGCTTTTGATCAATTC
TTGAAAAGACTTACTCTGAATCACCATTTATGTGGATTGAAACCAACTCTTTCTTCAAGTTAGCTGAC
ACCTCAGATCCAAATTGGTGGTTCTTGATACCTGGAGACCTCTCCACCTGACTTGTGATCTCCAC
TACGACCTAATCAAGAGTGGATGTAGTGAGATGAAACCTGTAAGGGTGTATCCCTTATTGGACACTATGGGAGA
TCCAGTTAATGCCCTTAAATCTTGTGAAAGTATGAGCTCTGCTGATCTGAGCTGAAAGTTTGATATGAT
AGCAGTGCACCACTCTGCTGCACTCAAGGGTTGTCTCCAGAAACAGAGACATTCTTCTATATAATGG
AAAACAGATTCCCATAGGACCCATTCTGCTGAAAGGGGATCGAACGTTGCAAGTGGCAATTTCAGGATTCTGAC
GAACACATGGGAAGAAACTCCAAACCCAGCTTCAACAGTGTGCTATCTGTTTCTCTATGGTTCTAGCTCTG
AATGGGGTACTGTAGCAGACAACTCACAGTGAGGCTTTGTAATCACGGGAGACTACAAATACACAGAGCTG
CAGAACTTAACTACAGGTTCAACCCCTAAGTGAGACATGTTCTCAGGATGCAAAGGAAATGCTACCTCGT
GGCTACACATATTAGAATTAATGAGGAAGGGCTGAAAGTGCACACAGGCCCTGATGTA

FIGURE 70

MELVRRLLMPLTLLLILSCLAEIIMAEAEAGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPERENKSIRIIIFSYVQLDPDGSCSESENIVKFVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDITLEGSFTSPNYPKPHPELAYCWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVL
TDYANSYRGFSASYTSIYAENINTTSLTCCSDRMRVIIISKYLEAFNSNGNNNLQLKDPTCRP
KLSNVVEFSPVPLNGCGTIRKVEDOSITYTNITFSASSTSEVITRQKQLQIIVKCEMGNST
VEIYYITEDDVIIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFOFNNAFKFLRSMSVYL
QCKVLIICDSSDHQSRCNQGCVSRSKRDIISSYKWKTDSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFFNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGGAGCCTGCAGAGAGGAACAGCCGCCCTGCC
GGACATGCGGGCCCCAGGAGCTCCCCAGGCTCGCGTCTCCCGTGTGCTGTTGCTGTC
TGCTGCCGCCCGCCGCTGCCAGCAGCGCACGCCAGCGCTTGACCAGGCCAGTCGGCATCTTCA
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAGTCGGCATCTTCA
GGGAGTGTTTCCGTGCCAGCTTCCGTAGCGAGTGTTCTGGTGGTATTGGCAAAAGGAAA
AGATAACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTACAGAAAATTTTAATGCCAACAGTGGGAGATATTTCAGGC
CTCTGGTGC_{AA}ATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGT
CAAATACTTCTGGAACTTGGAACTGCCATAGATGAGGGGCCAAGAGGACATTGCAAGGAA
CTTGAGGTAGCCATTAGAACAGAACACTGCCATTGAGCTGTACTATTCCCTTTGAA
ATGGTTCATCGCTTCCCTGAGGATGAATCCAGTCATTCCATAAGCGGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTAGTGAACAACATCAGCCTGAGGTCTGTGG
CTCGATGGTACGGAGGCCAGCGATCAACTGGAACACAGCACAGGCTCTGGCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCACTGATCGTTATAACCCAGGACATCTTGTCCA
CATAAATGGGAAACTGCACTGACAATAGACAACACTGTCCTGGGCTATAGGAGGGAGCTGG
AACTCTGACTATTCAATTGAAGAATTGGTAGGCAACTTGTAGAGACAGTTTCACTGTG
GAGGAATCTTGTGAATATTGGGCCACACTAGATGGCACCATTTCTGAGTTTGTGAG
GAGCCACTGAGGCAAGGGCTGGCTTCTGGCTAAAGTCATGGAGAAGCTATTGAAACCTA
TACCTGGCATCCAGAATGACACTGTACCCAGATGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCCTAAATGGGCCACATCAGGACAGCTTCTGGCCAT
CCAAAGCTATTCTGGGGCACAGAGGTAAACTACTGGGCCATGGACAGGCCACTTAACTG
GATTCTTGGAGCAAAATGGCATTATGGTAGAAGCTGCCACAGCTAACCATTCATCAGATGC
CGTCTAAATGGGCTGGCTTCTGGCTAACATATTGTGATCTAAAGTGCAGACTGGCTG
ATGCTGCAAGTTGTCTAAGGCTAGGAACATCAGGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGAACTGGATAAAATTATTGGCAGTGTACCCCTTCCCTTTTCCACTA
AATTTCCTAAATTACCATGTAACCATTTAACCTCTCAGTGCACITTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACACTGAAAATTCTGGTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCCTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGACTGTATTACAAATCTAGATGCCATAGCTTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAACAGCATGTTACTG
AATACTGTAGGCAATAGTAAACAGTGTATTGTATATCGAACACATATGGAAACATAGAGGAAG
GTACAGTAAAATACTGTAAAATAAATGGTCACCTGTATAGGGCACTTACCAAGTGGAG
CTTACAGGACTGGAAGTTGCTCTGGTGAAGTCAGTGAAGTGAATGTGAAGGCCCTAGGACATTA
TGAACACTGCCAGACGTTATAAAATACTGTATGCTTAGGGTACACTACATTATAAAAAAA
GTTTTCTTCTTCATTAAACATAAGTGTACTGTAACCTTACAAACGTTTAATT
TTAAACCTTTGGCTTTGTAAATAACACTTAGCTAAACATAACTCATTGTC
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTEWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPFGSEWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFLGYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHWKENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCCGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

TOP TO RECEPTOR

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

ACGAGGGAAATCCGGATGTCGGTTATGAAGTGGAGCAGTGAGTGTGAGGCCAACATAGT
TCCAGAACTCTCATCGGACTAGTTATTGAGCATCGCCTCTCATATCACAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCAGGTGCTTCAGGCTGGTGTG
CTTCTCACTTCATCTGGACACAGGGCTCTGGTCCAAGGCTTGGCTGAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTGTGAGCAAAAAGGGCAACCAGC
AGCTGAATTCAAGAAGCTAAGGGGCTGTAGGCTGCTGGACTAAGTTGGCCGGAAG
GACCAAGTGAACAGCCTTGAAGGCTAGCTTGAACCCAAACCCAAAGTGTGGAAAAATGGGTGGGTG
TGGATTCTGTTGTCATCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTGGGTG
TCCTGATTGGAAAGGTTCCAGTGAGCCAGTGTGAGCTTGGAGCTATTGTACAACCTGTAT
ACTTGGACTAACCTGTCATTCAGAAATTATCACCAACAAAGATCCCATAACTCAACACTCA
ACTGCAACACAAACAGAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCT
ACTCTCAAATACCTGGCCCTACTACTACTCTCTGTCAGCTCCACTTCTCACCG
AGAAAAAAATTGATTGTCAGAAGATTTTATGAAACTAGCACCATGTCTCACAGAAC
TGAACCAATTGTTGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTGAGTGTCTCTCTCTGGTGTGAGCTGGTCTGGATTG
TATGTCAAAAGTATGTCAGGCCCTTCTTACAAAGAACAGAACAGGAAATGAGGAAATGAT
CGAAACCAAAAGTACTAAAGGAGGAGAAGGCCAATGATACAACCCAAAGAACAGGAAATGAT
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGCAGTGCCTGGAA
GCTGAAGTT**TAGATGAGACAGAAATGAGGAGACACCTGGAGGTGTTTCTTCTGCTCC**
TTACCCCTGCCCCAGCTGGGAAATCAAAAGGCCAAGAACCAAAGAACAGGAAATGTCACCCCT
GGTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGACCAAAGAACAG
CCCTCTCTTATTGTAACCCCTGCTGGATCTATCCTCTACCTCAAAGCTTCCACGGCC
TTCTAGCTGGCTATGCTTAAATATCCACTGGGAGAAAGGAGTTTGCAAAGATGCAA
GGACCTTAAACATCTCATGCTTACAGTACCTGGTAAAGGCCCTCCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCCTCTCTCAGCTCTGACATGGGAGAACAGTATCCCACCTGACATGCTTCTGAGGCCGGTA
AGAGCAAAGAACAGTGGCAGAAAAGTTTAGCCCCGTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTGTAAGCTAAATAAAGAACATAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTGTTTCTCTGAACACATTGAGGTGGA
ATCAGTGTAGAACACACACTTACTTTCTGGCTCTACACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAAACAAAATAAAAACCTTATAAAATTCTATTCTATGTA
GTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATGCACTAGTAAAGCCTATCTGGAGCTATTCT
GTTTGATATTCTAGCTTACTCTTCAACTAATTTTATTTGCTGAGACTAATCTT
ATTCATTCTCTAAATATGGCAACCTTAAACCTTAATTAAACATACCTAAGAAG
TACATTGTTACCTCTATACCAAGGCACATTAAACCTTAATTAAACATACCTAAGAAG
GCCCTCTTTTCAACAAGAAGGGACTGAGAGATGCAAAATATTGTGACAAAATTA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNNPKCGKNGVGLIWKVPVSRQF
AAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCAATTGCTCTCGTGTTCGGTGCCCGGACTTACGATGG
CTCGCCCAACCTTACTACCTCTGTCGCCCGCTGCTCTGCTGCCCTCCTACTCGTGAGGAA
ACTGCGCCGCTGCAACGGCTGCCCCAACCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCTGATGTTCTCAGTGCCTTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCTGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCGCTGGATATTGCACTGGGCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACAGAACGGGACAAGAGGGTCACTTGGATTGGAGTTCTTGCAA
TTGGCTAATGACTGCCAACATTTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACCGGTAC
AAAGTGAGCACATCCCCCTACCAAGCAACTCCCTACCCGTATCCTGTTCAAGGGCAA
GGAGGCAATGGCGGCCACAGATTGACAAGAAAGGACGGGCTGCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTAACCCCCACACAGTGTCA
GGGGAAAACAAGAAGGATAAATAGATCCTCACTTGGCAGTGCTCCCTCTGCAATT
CCAGGCTCTTCCATAACCAAGCCTGAGGCTGCGAGCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGGCAGCATGCGAGCTCTGATTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGAAATGGTTCCCAAGCTGGGTCAGTGTGTTAACTGCTTATC
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTCCCCAAGGACTCTGCTTCAAGCCCTCTGCTTGGATTGGTC
TTCATAAAAGATAAGCTAACCTTGCGCTAGCTAACGGAGAACCTTAACCAAAAG
TTTTATCATTGAAGACAATTGAACACCCCCCTATTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAACCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCAACCCAGTTGATGGCTTCCGTAATAAAAGATTGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAFLVRKLPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFMSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

FIGURE 78

MGLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLNLGVKLVVEETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYCEVIDGLEDESGLVELELRGVVF PYQSPNGR YQFN FHEGQQ
VCAEQAAVVASFEQLFRAWEGLDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKG R VVY LEHPEKLT LTE AREAC QED DATIA KV GQLFAAWKF HGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGCCGAGGCCCTATGGC
CAGGGGAGGGTGCACCAGCGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCAGTACGACCATGAGGCTTCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAGCCAGGCCGCTGGGGCGATCGTGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTCGCGCGTGGATCGGCACACGCAGCGGC
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGACGGGCGTGG
GTTGGGAGGGAGCTGCGAACGCCACCTATGGCCACTACCGCAGGGTGAAGAATTTCATGAC
GTGGAGGATGCGAGAGACCTACAAAAAGATGCTGGCTGGGACGGAGCGCGTTCCGGGTGGC
CGACCCAGGATGGGACTCGATGCCACTCGAGAGGGAGCTGACGCCCTCTGCACCCCGAGG
AGTTCCCTCACATGCCGACATCGTATTGCTGAAACCTCTGGAGGACCTGGACAGAAAACAAA
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGGCCCTGGGAGGA
GGAGCCGGCGTGGGTGCAACGGAGAGGCAGCAGTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGGGTGGGCCACTGGGTGCTGCCCTGCCAGGACGCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCTGGTAATTGGAACATGTTTGTTGGCAGTCAGGCCACCAACTATGGCAGG
ACCTGACCCGGCACCAAGATGAGCTGTGAGCACCAGCACGCCACAGCCTCAGAGGCCG
ACAATGACCGGAGGAGGGCCGCTGTGGTCTGGCCCTCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCCTGCCCTGGGCTCTCAGGGACCCCTGGGTGGCTTC
TGTCCTGTCAACCCCCAACCCAGGGAGGGCTGTCTAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGGCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCACCACATAGACTGAAACTCCCT
GGCCCCAGCCCTCTGGCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLRLRGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAEELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCGGGGTGGAATCTGAGCAGGTGCGGAGCCCCGG
GCGGGCGGGCGGGGTGCGAGGGATCCCTGACGCCCTGCTCCCTGTTCTTGCGCTCCCAG
CCTGCTGTCGCTGTTGGGCCCGCCCTCCCGGGTGCAGGGGTTGACACCCGATCCTG
GGCCTCGCTCGATTGCGCCGAGGCCCTCCAGACCTAGAGGGCGCTGGCCTGAGCAG
CGGGCTGCTGTCGCTCTCTCCCTGCGCCGGGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACCCGCGGGGCTCCCGCACCTGGCTTGGCCATTCTCCCTCTCAG
GTGTGAGCAGCCTATCAGTCACC**ATGT**CGCAGCCGGATCCCGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCCGGGCAGCAGGGAGCCCTCCATTGCTATACATG
TTTACAGAGGGCTGGACATCAGGAAAGAGAACAGATGTCCTCTGGCCTGGC
CTCTGGAGGAATTCTCTGTATGACATAGTATGCTTCTGTATCAGCATATG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TTGGCTGAGAAAATCTTCACTGAGTGGCAATGCCACTGGCTCAATAGCTTTAGAT
GGTCTGCTTCTTCACTAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGACTAAAGAAACACCCGAGAAGAAAATGG
CAATAAGATTGTAAGCAGACATTCGATTTCTGATTGATGGAAGCTTTAATATTGGCAGC
GCCGATTAACTTACAGAAGAATTGTTGGAAAGTGGCTTAATGTTGGAAATGGAAACA
GAAGGACCATGTTGGGCTTGTCAAGCAGTGAAACATCCAAAATAGAATTTCAGGGGTA
AAACTTACATCAGCCAAGATGTTTGTGCAAAAGGAGTAGGTTCAAGGGCT
ATTCCAATACAGGAAAGCCCTGAAGCATACTGCTCAGAAATCTTACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCAAAGTGGTGGTGTGTTATTGATGGTTGCCTTCTGATGACAT
CGAGGAAGCAGGGATTGTCAGAGAGTTGGTGTCAATGTTAGTTCTG
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGGCTGCTGT
CGGAATAATGGCTTCTCTTCAACATGCCAACCTGGTGGCACACAAAATACGTA
GCCCTGTTGACAGACTGTCACTGATGAAACATGATGTCAGCAAGACCTGTTAAACT
CAGTGAACATTGCTTCTAATTGATGGTCCAGCAGTGTGGAGATAGCAATTCCGCTC
ATGCTGTAAGATTGTTCCAACATGCAAGACTGGAAATCTGGACATTGGTGGCAAGAT
AGCTGCTGTAAGCTTACTTATGATCAGGCCACGGAGTTCACTGACTATAGC
AAAGAGAATGCTCTAGCTGTCATCAGAAACATCCGTATATGAGTGGGAACAGCTACTGGT
GATGCCATTCTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCCTAGTAATTGTCACAGATGGCAGTCATGATGTCAGGGCTTCAAGGGCTTGCAGCTG
CACATGTCAGGAATCACTATCTCTGTTGTTGGCTGGCTGGGACCTCTGGATGACCTG
AAAGATATGGCTCTAACCGAAGGAGTCACGCTTCTTCAAGAGAGTTCAACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGGATTGAGATTCTTGAATCCAGCAAT
AATGTTAACATTGACAACTGAAAGAAAAGTAGCAAGGGGATCCAGTGTAAATTGATT
CTCTATAACTGAAATGCTTAGCATACTAGAAATCAGATAAAAATATAAGTATGTCAC
AGCCATTAGCCAATAAGCACTCCCTTAAGGCCCTGCCTTCTGGTTCAATTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACACTCAGGAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCAACCATGCTACTAAATGACAGATATGCAAA
TTCCATAGCTCAATAAGAATCTGATACCTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSI CGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPVHGLVQASEHPKIEFYLKNTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNFIIVSVAKPIPEELG
MVQDVTFVDAVKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNAFLI
DGSSSGDSDNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGCACCCGGGGCCCCACCGCGGCCCTCCGCATCTGCACCCGAGCCC
GGCGCCCTCCGGGGAGCAGCATCAGTCAGCGCCCGCAGCGCAACTCGGTCCAGTC
GGCGGGCGGCTCGGGCGAGAGCGAGATGCAGCGCTTGGGCCACCTGCTGCTGC
TGCTGGCGGGCGGTCCCCACGGCCCCCGCAGCGACCTCGGCTCAGTC
AAGCCCGGGGGCTCTCAGCTACCCGGAGGAGGAGGCCACCTCAATGAGATGTTCCGC
GGTTGAGGAACCTGATGGAGGACACGCAGCACAAATGCGCAGCGGTGGAAGAGATGGAGG
CAGAAGAACGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGCCAAACTTACCTCCAGCTAT
ACAATGAGACCAACACAGACAGAACGGTTGGAATAACCATCTGACCCGAGAAAT
TCACAAGATAACCAACAAACAGACTGGACAAATGGCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAACGGAGAGCACAGGAGCTGTCATCATCGACAGGACTGTGGGGCCAGC
ATGTAUTGCCAGTTGCCAGTCCAGTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT
CTGCACCCGGGACACTGAGTGTCTGGAGACAGCTGTTGCTCTGGGGTCACTGCCACAAA
GGTGCACCCAGGGGGCAGCAATTGGGACCATCTGCAACACCAGGGACTGCCAGCGGGCTG
TGCTGTGCCCTCAGAGAGGCCCTGCTGTTCCCTGTCACACCCCTGCCGTGGAGGGCGA
GCTTGTGCCATGACCCCCGCCAGCCGGCTTCTGGACCTCATACCTGGAGCTAGAGCTGATG
GAGCCTTGGGACAGTCCCTGTCAGGCTCTCTGGCAGCCCCACAGCCACAGCTG
GTGTTATGTCAGGCCAGGACCTCTGGGAGGCCCTGACCAAGATGGGGATCTGTC
CAGAGAGGTCCCCGATGAGATGAAGTTGCAGCTTCATGGAGGAGGTGCGCAGGAGCTGG
AGGACCTGGAGGAGGACTGACTGAAGAGATGGGAGCTGGGGAGGCTGCCGTGG
GCACTGCTGGGAGGGAGAGAGATTTAGATGCCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTCGCTTAAAGCTGGGCTGACCAAGCTTCTTAC
TCTCTTCCAGTAAAGTTTCCCTCTGCTTGACAGCATGAGGTGTTGTCATTGTTCTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTCTGGAGAGTCAGGAGGGTTAAAC
TGAGGAGGAGCTGGCCACCCCTGTCAGGATTATTGGCTCTTGGCTTACAGTGGCAG
ACAGCCGTTGTTCTACATGGCTTGTATAATTGTTGGGGAGGAGATGGAAACATGTT
AGTCTCCCTGATGGTTTGGGAAATGAGGAGATGGGGAGGAGCTGGCAAAACATCAA
CTCTGCCAAAATGCAACAAATGAATTTCACCCAGTTTCCATGGCAGTGGTAAGCTG
TGCTTCACTGAGTAAATGTTCTGAGATGAAATGTTCTGCTTACCCCTGCAATTACATGTT
ACCAAGTGTGTCAGCTACCTCTGTCAGGCCAGGAGCTTCTACATCCAGATCAATT
CCTCTCAGCACACGGCTGGGGAGGGGGTCACTGGCTCTCTGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTACACAGCTGAGAAGACAGAGCAGTTCT
CTGGTTGTGACTCTAACGTCAGTGTCTCTCCACTACCCACACCAGGCTTGGTCCACCAA
AAGTGTCCCAAAAGGAAGGAGAATGGGATTTTCTGAGGCATGCACTCTGGAAATTAAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAACACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCTAAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT
TGCATTAGTAACCTTGAAGGTTATGACTGAGCTAGGACATCAGGTTAACCTGCAAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTAAATGAAGATTGCAAAATCACTTAGCAGCAAC
TGAAAGACAATTATCAACCACGTGGAAATAACCAACCGAGCAGGGCTGTGAAATGTT
GTAAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTC
TGGACTGTTGCCACCATGTATTCTCAGAGTCTTAAAGTTAAAGTTGACATGATGTT
TAAGCATGCTTCTTGTAGATTAAATTATGATAACATAAGTTGCAATTAGGTT
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAKASSEVNLANLPSPYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGNSGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLLVAPLLLAWAGATATPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLQLQSNSIVRVDQSELGYLANLTELDSLSQNSFSDARCDPFLALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLIELMIGGNKVDAILDMNFRPLANLRSVLAGMNLRREISDYALEGLOSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLINKNPLQRVGPQDFANMLHLKEGLLNNMEELVSIDKFLAVNLP
ELITKLDITNNPRLSFIHPRAFHLPQMELTMLNNNNALSALHQQTVESLPNLQEVGHLHGNNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVFPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPPEPEIYWVTPAGLRLTPAHAGRRYRVVPEGTILELRRVTAAEAGLYT
CVAQNLVGDATTKTVSVVVGRALLQPGRDEGGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLWPWNPKRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

FIGURE 88

MRQTIIKVIKFILIICTVYVYVHNIKFDVDCTVDIESLTYRCAHPLATLFKILASFYI
SLLVIFYGLICMYTLWWMLRSKKYSFESIREESSYSIDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQIQLNNNEWTLDKLQRQLTKNAQDKLELHLFMLSGIPDVTVDLVELEV
LKLELIPDVТИPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRVIVIDGLRELKRLKVRLKSNLSKLPQVVTDVGVLQKLSSI
NNEGTTKLIVLNSLKKMANLTELLELIRCDLERIPHISIFSLHNLQEIDLKDNNNLKTIEEIIISFQ
HLHRLTCLKLWYNHAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNQLQNLAITANRIETLPPELFQCRKLRALHGNVLSQSLPSRVGELETNLTQIE
LRGNRLECLPVELGECPLLRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTGCTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTTATTATGCCACCAACTCTGCAAGAACTTCTCAGAACACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGCTTAGCAGTGGATTGGAAACTTGGAGGAATTGGGC
CCCTTGACAGTGTCTCAACCACGGAAAACCACCTGGTCCAGGCTGCCAGTCTCTTATT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTCTCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGACCTTATAAGGCCATTAGCAGGGACCATCAAGTGAACCTTGCGGGGGT
TGCCCTGGGTGATTCCCTGGATCTCCCCCTGGTGAATTGGCTCTCCTGGGACCTTAACCTGT
ACAGCATGTCTTCTCGAACAGAACAGGCTGGCAGAGGTGCTAAGGGTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACAAAAGCACTCCCA
CGTCTACAATGGAGTCAGCTAGAACATTCACAGAGCCACCTAGTTGTCTTGTCAGCGC
CACGTGAGACACCTACAAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAATTATTCCTGGAGGATCAATCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGGTGGAGGCAGGGATC
AACGTGACGGGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG
GGTGGGAAACTGAAGTGGCCAGAACACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGAAACATCTGCTTTGTCAAGTCCCTACAAGAACCTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTCTTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGGACTCAGCAAGAAAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGACAGAGGATAAAATCATTGTCT
GGAGGCAATTGGAAATTATTCCTGCTTCTTAAAAAAACCTAACAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIIGPLDSLKPRKTTWLQAASLLFVDNPVGTFGSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVSLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLNAVNKGLYRE
ATELGWKAEMIIIEQNTDGVNFYNIITKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWALKALYSDPKSLETSAFVKSYKNLFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGCCGA
CGGGTCACTACGTGCATCGTGGGTGGAGAGGACGCCAAGTCGGCGTTGGCGTGGCA
GGGGAGCCTGCCCTGTTGGGATTCCCACGTATGCCAGTGAGCTGCTCAGGCCACCGCTGGG
CACTCACGGCGGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGAGCCTGCAGGCCACTACACCCG
TTACTTCGTATCGAACATATCTATCTGAGCCCTGCCTACCTGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGCTGCACCTGTCACCTACACTAAACACATCCAGCCATCTGCTCCAG
GCCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCCCCAACCCCTCCAGGAAGTTAGGTGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCAAGTACAGTTCCCAAGGACATCTTGGAGACATG
GTTTGTGCTGCAACGCCAACGGCGGAAGGATGCCCTGCTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCAACTTGAGTGGATCCAGAAG
CTGATGGCCCAAGGTGGCATGTCACGCCAGACCCCTCTGCCACTACTCTTTCCCTCT
TCTCTGGGCTCTCCACTCTGGGCCGGTTGAGCCTACCTGAGCCCATGCAGCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCCTTGCGAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW
DSHVCVGVSLLSHRWALTAACFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLsapVTYTKHIQPICLQASTPEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVEQVAAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSVGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCCACCGCTCCGGGACCGCTGGGAAGGGCAGA**A**TGGGACTCCAAGCCCTGCCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGGCCGGAGCCGACCAGCGAGGACGC
TGGCCCCAGGCTGGGTGTCCTGGGCCGTCGGACCCCTGAGGAAGAGCTGAGTCACCTTT
GCCCTGAGACAGCAGAAATGTGGAAAAGACTCTCGGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCCATACTACGGAAAATACTCTGGCTAGAGAATGTGGCTGATCTGGTGGAGGCCATCCC
CACTGACCCCTCACACGGTGCAAAAATGGCTTGGCAGCGGAGCCAGAACAGTGCCTATTCT
GTGATCACACAGGACTTCTGACTTGTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCC
TGGGGCTGAGTTTCACTATGTGGGAGGACCTACGAAACCCATGTGTAAGGTCCCCAC
ATCCCTACAGCTTCCACAGGCCCTGGGCCCCCATGTGACTTTGTGGGGGACTGACCCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGGCCAGGTGACAGGGACTGTAGGCC
GCATCTGGGGTAACCCCTCTGTGATCGTAAGCGATAACAATTGACCTCACAAGACGTGG
GCTCTGGCACCGAACATAACAGCGAACAGCTGCGGCCAGTCTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCTGGCCCTCTGGGCAAATTGTCACATCAGGATCAGTAGC
CCGTGTGGTGGACAACAGGGCCGGGGCCGGGGGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGAGTGAAGTGTGCTGGTGCACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGGCCCTTCTGGCTAGTGGCTCATCTGCTCAGTAATGAGTCAGGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCACGCGCTACATCCAGCGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTTCGCCCTCAGGTGACAGT
GGGGCCGGGTGGGTCTGTCTCTGGAAAGACACCAGTCGGCCCTACCTTCCCTGCCCTCCAG
CCCTATGTACCAACAGTGGAGGACATCTTCCAGGAACCTTCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGGGTGGCTTCAGCAATGTGTTCCACGCCCTCATACCAAGGAG
GAAGCTGTAACGAAGTCTCTGAGCTCTAGCCCCCACCTCCACATCCAGTTACTTCATGC
CACTGGCCGTGCTTCTGGAGATGTTGGCTGCACTTCTGTGACTGCTACTGGGTGGTCAGAAC
GAGTGCCCATTCATGGGTGTCGGAAACCTGGCCCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCTTAGTGGCCGCCCTCTTGCTTCTCAACCCAG
GCTCTACCGAGCACGGGGTCTCTGGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGGTAGAGGGCAGGGTTCTGGCTCTGGCTGGGATCTGTAACAGG
TGGGGACACCAACTTCCCACCTTGCT**G**AAGACTCTACTCAACCCCTGACCTTCTATC
AGGAGAGATGGCTTGTCCCCCTGGAAGCTGGCAGTTAGTCCCTTATTCTGCCCTGTG
GAAGGCCCTGCTGAACCCCTCAACTTGTACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCCTGTGAGCTGACTTCACTTCCACCTCATGCTCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGATTTTGAAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTTCCAAGGGTTGATACAGACTCTGCACTA
TTCACTTGATATTCACTTCCCAATTCACTGCAAGGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAAATGGCTCCAGTGCACTACTCTCATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCTTACTTACCTTCCAGGTCTTAACCTCTG
ACTACTCTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG
TCCATTGCTAGATTGGCTTCTCTCATGTTACTCATGTCCTCCAGAACAAATCACTGACA
TCTACAAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA
TGAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELS LT FALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRSPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTEHVVRSPHPYQLPQALAPHVDFVGGHLHRFPPTSSLRQP
EPQVTGTVGLHLGVT P S V I R K R Y N L T S Q D V G S G T S N N S Q A C A Q F L E Q Y F H D S D L A Q F M R L F G
G N F A H Q A S V A R V V G Q Q G R G R A G I E A S L D V Q Y L M S A G A N I S T W V Y S S P G R H E G Q E P F L Q W L M L
L S N E S A L P H V H T V S Y G D D E D S L S S A Y I Q R V N T E L M K A A R G L T L F A S G D S G A G C W S V S G R H
Q F R P T F P A S S P Y V T T V G G T S F Q E P F L I T N E I V D Y I S G G G F S N V P R P S Y Q E E A V T K F L S S P
H L P P S S Y F N A S G R A Y P D V A A L S D G Y W V V S N R V P I P W V S G T S A S T P V F G G I L S L I N E H R I L S G
R P P L G F L N P R L Y Q Q H G A G L F D V T R G C H E S C L D E E V E G Q G F C S G P G W D P V T G W G T P T S Q L C

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCCGGCGCCACACCTGTCTGAGCGCGCAGCGAGCGCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCCTGGCATGGCAGGGATTCCAGGGCTCTTCTCTC
TTCTTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTAACAGTGCCCCCTGGAAACCACTTG
GCCTGCATACCGCCTCCCTGCTTGGCCAGTCACTACCCCTAACATTAGCCAAGCCAGACT
TTGGAGCGAAGCCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTATAAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCGCACAGAGACGCAGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCTGGTGCAGAGAACGATGTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGAACCCAGAACGCTTCAGTGGCTTCCATAAGCCC
AAGTTAAAGATGGTGGTCAGGGGCCAACGACTCCACTCAGCCATGCCAGACATGAA
ATTTCACTGGGATCCGGGTGAAACGCACCCATGTGCCAACGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAGCCCCACAAGGAAAAA
TTTATGAAGATTGGGGTGAACCTCCTGCTAAGCAGCTGCCAGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACACAGGCAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTGCTCTACCAAGCAATGCGATGCCAGGGCAGGGCTGGGCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACAGTGGGAGCAGAAAATTATGGCATTTCAGG
GCACCAAGTGGGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGAACACAGTGTCCCTCTGGCAGCAATTAAAGGCTCTCATGTTCTTATTAGGAGAGGC
AAATTGTTTTGTCAATGGCGTGACACGTGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATTTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTCACGTTTG
CAAACATTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATTTGACAATCTCACGTTTG
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLFLCAVGQVSPYSAPWKPTWPAYRLPVVLQPSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPPLTYEEAKQYLSYETLYANGSRRETQVGIYILSSSGDGAQHRDSSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPDKDGGRGANDSTSAMPQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPKHKKRKFMKIGVSPPAKQLPGGRIHFGYDNDRPGNLVYRFCDVKDETYDLYQQCD
AQPGASGSGVYVRMWKRQQQWERKIIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCGCTCCCCGCCCCACCAAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCA
GCAGCTGAACGGGTTGTGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAAATGGGACCCACCACACTGCGCAGGTTCTGCTCACCGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCTGGCTCTCGTCCCAGAAGGTGGGTGTGCTGGTGGAGC
CCCACCTGTGATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTGAG
CGCTCCATACAGTTCTCAGAGCGGGCTCTGCCATCTGCCACCTGATGCCCTATCCACCT
CCCTCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTG
CCCACCTCAGACCCCTGAGAACGCTGAAGGTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGACG
GCCCTGGCTGCTGGCGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGTCTACATCAGCCTCTGCGCACCGCTGGGTGGAGAACATCGCAAGGGTGCA
GCTCCGCGGGCGCCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGCGCCTCTAGGGCGCAGCGGACGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGCGGCCCTCGGGCGTTTCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGGGAAAGGAAACCCCTCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCTCATGTCGGGCCAC
GACTTCCGGCCCGCCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTGTAAACCTGCCACATATCTTATTCTCCAATTCAATAAATTATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVGSGAPPALGGGCLGTTSLLLAASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSLRWVITAHHCFKDNLNPKYLFVLLGAWQLGNPGSRQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSEVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCACCATGCACGGCTCTGCAGTTCTGATGCTCTGCTGCCGTACTGCTA
CTGCTGGTGGCACCAACAGGCCCGTTGGAGCCCTCACAGATGAGGAAGAACTGTTGATGGT
GGAGCTGCACAACCTCTACCGGCCAGGTATCCCCGACGCCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCCTTCGCCAACGGCTACGCAGGCAGTGCCTGGGGCAC
AACAAAGGAGCCGGCGCCGGCGAGAACTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTAGGACTACAAACCTCAGGCCGCCACCT
GCAGCCCAGGGCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCAAGACAGAGGAGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCGGGGAACTGTAAGGGAAACGCCCTACAGGAGGGACTC
CGTGTCCCCTAGTCCCTGGCTACCACTGCAAGAACCCCTGTGAACCCATCGGAAGC
CCGGAAAGATGCTCAGGATTGCTTACCTGGTACTGAGGCCCCATCTTCCGGGCACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCTTCTCCCTAGCAACGGGATTCCGGTTCT
TGGTAAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTGCTGCTGTGGAAACCCAGGCC
CCAACCTCCTAGCAACGAAAGACCGCCCTCATGGCAACAGAGGCTCACCTGCTAAC
AACTGAGGTCCCTCCATTGGCAGCTACAGCCTGCCCTGGATGAGGAGGCCAGTTA
CTTCCCAAATGACCCATGTTCTATCCAAAATCAGCAGAACAGTACAGACAAAACA
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTCTGGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGTGAGGCTGAGGCTGAGTTGCCCTCTCAGTG
AGGTCTGGCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCTCCAAGTCCCTGCCAATTTCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCCTGGCTCTGCAGTCGCTTGCAGGTGAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGCTGAACCTGGGCCCTGGTATGTGTGGGCCCTCTCTGGGA
CTACTGCTCTGCCCTCTGGTGTGTTGGCTGGAATCTTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCACTGTCCTCTGTATCTCCCCACCCCTGTCCCCAGCCCTAAACAGATA
CTTCTTGGTTAAAGGCCCTCCGGAAAGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC
ATCCTGGAGGCCACAAGGCTGGCTGGCTGCCAGCTCAGGAGGCCCTGAGGACTGCCACACC
GGGGCCACACCTCTGCCCTCCCTCTGGCTAGTCCTGGGGTGGAGGATTGAGGAGCT
CACTGCCCTACCTGGCTGGGCTGTCTGCCACACAGCATGTGCCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCTAGGGCAGGACGAGGAAGGAAAGTAACCTCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVCWGHNKERGRGENLFAITDEGMVDPLAMEEWHEREHYNLSAACSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVVEETNIELLVCNYEPPGNVKGKRPyQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETOAPTSLATKDPMSMATEAPPCVTTEEVPSILAAHSLPSLDEEPVTFPKS
THVPIPDKSADKVTDKTKVPSRSPENSLDKMSLTGARELLPHAQEEAEAEALPPSEVLAS
VFPAQDKPGEQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEQPDKPSVV
SGLNSGPGBVWGPFLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

FIGURE 102

MVDVLLFLSCLLFHISRPDLNRLSFIKASSMSHLQLSQLREVKLNNNELETIPNLGPVSA
ITLSSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLVLKLNLRNRIASIAPPKMFKLPQLQHLELRNRIKKNVDSLTFQGLGALKSLKM
QRNGVTKLMGAFWGGLSNMELIQLDHNNLTEITKGWLYGLLMQELHLSQNAINRISPDAWE
FCQQLSELDLTNHLRSRLDDDSFLGLSLLLNTLHIGNNRNSVYIADCAFGLSSLKTLDLKNN
ISWTILEDNGAFSGLDKLRLILQGNRIRSITKKRAFTGLDALEHLDLSDNAIMSLQCNQAFSQ
MKKLQLQHLNTSSLCDCKLKWLPQWVAENNFQSFPVNASCAPHQPLLKGRSIFAVSPDGFVCD
DFPKPQITVQFETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEHENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPPAPQIAWQKDGGTDFPAARERRMHVPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSI SANATLTVLETPSFLRPLLDRTVKGETAVLQCIAAGGSPPPKLNWTKDDSPLVVTER
HFFAAGQNLLIIIVDSDVSDAGKYCTCEMSNTLGTGRNVLSVIPTPTCDSPQMTAPSLLDDG
WATGVVVIIAVNCVVCTSLSWWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSQGTLLAD
RQDGYVSSESQSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCSPDPRTVLMDHYEPSYIKKKCYPCHSEESCRSFNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTGKALRRPHLDA
YSSFGQPSCDCQPRAFYLKAHSSPDLSGSEEDGKERTDFQEENHICTFKQTLENRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGGAGCTTTTTGGTGGTGGCTGTTGGGTGCCCTGCAAAATG
AAGGTGCAAGGACCGCAGCTTCCTGGAACCGAACGCAATGGATAACTGATTGTGCAAGAGAGAAGAAC
GAAGCTTCTTGTCAGGCTGATCTAACAAATGTGTATATGTGACACAGGGRCATTCAAGAATGAAA
TAACACAGAGTTAGACCCGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGTGATGGGAAATGAAGAACGGAGGATTCACAAAGAAAAGTATGTCATTCTC
TATAAAGGAGAAAGTGAAGCCAAGGGAGATTTTGGAAATGAAAAGTTGGGCTTTTTAGTAAAGTAAAGAAGT
GGTGTGGTGTCTTCTTCTTGAATTCCCAAAAGAGGAGAGGAAATTAATAATCATCTGCAAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGGGCAGATTGAGGCAATTGATTGGGAGAGAAACAGCAGAGCACAGTGG
TTTGTGCTTATGTGACTAAATTGACGGATAATTGAGTGTGATTCTCATCAACCTCTTTTTTAAAT
TTTATCCTTTGGTATCAAGATCATGCGTTCTCTGTGTTCAACACCCTGGATTTCATCTGGATTTGCT
GTGATCAGTCTGAATAACTGAGGAAATCCAGAACAGGAAACCCAGATAATTATGATGTTGAAAGAT
GACCTTACATCCACAGAGATAATGATAGGCTTAGGTTAACAGGCCCTGCTGTGTTGCT
GCTGGCTTCACCTCTTGTGGCTGGTCTGGTGCAGGCTCAGACCTGGCCCTCTGTGTCCTGAGCAA
CCAGTTCAAGGAGGATTTGTGTCGGGATGGTGGCATCTCCACACGGCT
GCTGAACTTCATGGTGAACCAAACTTCAGAGATCATCAAAGACTGAACAGCTTCAGACACTTGAGGACT
ACAGTGTGAGTGAACCAATCTGGGATTTGGCATCAGAACCTGGGCTTCTAATGGCTTGCGGAACCTCAACACTCTGG
ACTCTTGCACATCTGCTTACTACCACTCCCGAATGGACCTTGTGTTATGTTCTA
GGAAACACCCCCATTGAAAGCTCCCTTCTATGGCTTTAACAGAAATTCTCTTGTGCGGACTAGACTTGG
GGATTTGAAAGACTCTCATCTCATGGTGAAGGTTGTCGAACCTTGAGGTATTGAACTTGC
CATGTCACCTTCGGAAACTCTAACCTCACCGCTCATAAAACATGAGTGAACCTTCTGGGAAATCA
TTTATCTGCCCATCAGGGCTGGCTTCTGGGATTTGATGACCTTCAAAACTGTGAGTATGAGTCCCGAGAT
TCAGTGTGATGAACTGCGGTTCTGACACCTTCAGTCACTAGGGGATGACCTTACATC
ATTACTGTGCTCATGACCTCTCATCCTCCCTGATCATCTAGGGCAGATACATTACAC
TAACACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCGCTCGAACACAGCTTGTGCGGTTG
TAACACTCTCCCACTTAAGGGAGGTACATTGGAGAGCTGACAGAAATTCTACATGCTATGTC
GATTTGGAGGCGGCTGGAGACCTCAATGTGAGCTGGCAGTGGCTGAAATGTGGGGCTCCACATC
CTGACATCTGATCTGGATTACTCCAAATGGAAACAGTCAACGACATGGGGCTACAAAGTGGCGATAGCTGT
GCTGAGTGTGAGTACGTTAAATTCAAAATGTAACCTGTGCAAGATAACAGGCTGTAACATGTTGGTGGAGTAA
TTCCGTTGGGAAATACTGCTTCAGGCCACCTGTAAGTTACTCTGAGCAACCCACTCTCCTTCTTACTTT
AACCCTCAGTAGAGACTATGGAACCGCTCAGGTAGAGGACCGACAGATAACATGTTGGTCCACTCC
AGTGGTGCACTGGGGAGACCAACTGGGACCCACTCTCACACCCAGAGCACAAGGGTGCAGAGAGAAAACCTT
CACCATCCCGATGACTGATATAACAGTGGGATCCAGGAATTGATGAGGACTACAAAATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGTGTGTCATTCTCAACAGATGAGGAAGGAGCACCA
TCGGCAAAACCATCAGGCCACAGGACTGTGAAATTATTAAATGTTGGGATGATGAGATTACGGGAGACCA
CATGGAAAGCCACCTGCCATGCTCTATCGACATGAGCACCTAAATCACTATAACTCATACAAATCTCCCT
CAACACACAAACACAGTTAACACAAATTAATCTAACACAGTTCAGTGCAGTGAACCTTATTGATCCGAAATGAA
CTCTAAAGACAACTGACAGAGACTCAAAATCTAAACATTTCAGAGTTACAAAACAAACAAATCAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGGCTAACATTGTTCAAAAGTGTCTTACAAAAAA
AAAAGAAAAGAAAATTATTATTAAACATTGATGTCATAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQQIKVNSFKHLRHLLEILQLSRNHIRTIEGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDGLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKDELDSGNHLSAIRPGSFQGLMHQKL
WMIQSQIQVIERNAFDNLQLSVEINLAHHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCNDIL
WLSWWIKDMAPSNTACCACNTPPNLKGRYIGECDQNYFTCYAPVIVEP PADLNVTGMAAE
LKCRASTSLTSVSITPNTGVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNVGN
TTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVWDWETTNVTSLTPQ
STRSTEKTFTIPVTDINSIGI PGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTV EIINV DDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNISKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSPLRARAAAGLGLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCTTCRCLGDLDDCSR
KRLARLPEPLPSVARLDLSHNRLSFIAKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMMDGAFWGLSNMELIQLDHNNLTETIKGWLYGLMLQELHLSQNAINRISPDAWEFC
OKLSELDLTFNHLSSLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNNEIS
WTIEDMNGAFSGLDKLRRLIQLQGNRIRSIITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQQLHNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFCDF
PKPQITVQPETQSAIKGSNLFSICSAASSSDSPMTFAWKKDNLHHDAEMENYAHLLRAQGGE
VMEYTTILRLREVEFASEGKVQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPPAQIAWQKDGGTDFPAARERRHMVMPEDDVFFIVDKIEDIGVYSCAQNSA
GSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPQLNWTKDSLWVTERHF
FAAGQNQLLIIVDSDVSADGKYTCEMSNTLGERGNVRLSVIPTPTCDSPQMGTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITMTDETNLPADIPSYLSQGTLADRQ
DGYSSSESGSHHQFVTTSSGAGFQLPQHDSGGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSDPRTVIMDHYPESYIKKECYPCSHPSEESCRSFSNISWPS
HVRKLLNTSYSNEGPGMKNLCLNKSSLDFSANPEAVSASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

FIGURE 108

MEGEEAEQPWFHQWPWRPGASDSAPPAGTMAQSRLVLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFEEEEPVLVLSPEEPGPGLAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNQNNRLTSRGLPEKAFFEHTNLNYLYLANNK
LTLaPRFLPNALISVDFAANYLTKIYGLTFGQKPVLRSVYLHNNKLADAGLPDNMFNGSSNV
EVILILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDGLDN
ETFWKLSSLEYLDLSSNNLRSVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPAGLPRVRVTLMLHNQITGIGREDFATTYF
LEELNLNSYNRITS PQVHRDAFRKLRLRSLDLSGNRLH LPPGLPRNVHV LKVKRNEAALA
RGALAGMAQLRELYLTSNRLLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANA FDSTPNLKGIFLRFNKLAVGSVVDASF RRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCGGGCGCCGCGACGGACCTGCTCGGCCGCGCTCGCCGTGCTCTCCGGAGCGGCAG
CACTAGCCCCGGCGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCTCCATCGGGGCCACACCC
CAACCTGTTCTCGGGGCACTCGCGTGCGCCAGGACCCGCTGCCAACATGGATTTCCTCTGGCGCTGGT
GCTGGTATCTCGCTACCTCGAGGCCGAGCTGCGAGGGGGCTGGGGCAGGCAAATAGTGTCATCGAT
TGGCTATGTCGTTATGGTGGAGGATTGACTGCTGCTCGGGCTGGGGCTCGGGAGCTGGGACAGTGCAGC
TGTGTGCCAACCGAGTGCACAAACATGGTGAATGTCAGGCGCTGAGACAGTGCATCTGGTTATGCTGG
AAAACCTGTAATCAAGATCTAATGACTGTCGCTGAGGCCGCTGTAAGCACAGTGCATGAACACTTA
CGCCAGCTAACAGTGCCTACTGTCACAGGATAATGTCATGCCGAGGGTCTGCTCAAGTGCCCAGCTG
CTCCATGCCAACCTGTCAGTATGGCTGTGATGTTAAAGGACAACATGTCAGGAGGCTCTGCCCTAGAATT
GCACCTGGCTCTGATGGAGGACCTGTTGATGTTAAAGGACAACATGTCAGGAGGCTCTGCCCTAGAATT
TAGGCAGTGTGCAACATTGAGGACTCTGTCAGTGTGATGTTAAAGGCTTGCATCTCATGTTATGGAGG
CAAATATCATGTCATGACATAGCAGATGTCCTACTGTCAGTATCATGTCAGCAGCTTGTGTCATGTTATAA
CGTACTGGCTCTAACAGTGCACAAATGTAAGAAGGATAACAGGGTGAAGTACTGACTCTGTGTTATGCCAAA
AGTATGTCATGTCAGTCTCAGGCTAACATGTCAGGAGGAAATGGTACCATTTAAAGGCAACATGTCAGGAAA
TAATAATTGGATTCTCTGATGTTGAGAGTACTCTGGCTCTGGCAAGACCATATATTCTCTTATCATACCAA
CCTGCCAACAGAGCTCAGAACCTCTACCCACCTACACCCAGGAAACCCAGGACTGACAACTATAGC
ACCAGCTGCCAACACCTTGCAGGAGGATAACAGCTTGCACACAGGAGCTACAGACAGACCCCTCAGAAACCCAGG
AGATGTCGTTGTCAGTCTGTTGACACAGTTGTAATTTCGACCTGGTGTGATGTCAGGAGAAGACARA
TGACTTGCCTGAGGAAACATCAGGGGCCAGCAGCTGACAAATATCTGACAGTGTGCCAGGAAAGCCAGG
GGGAAAGCTGCAGCTGGTACCTCTGGGCCCTCATGTCATCAGGGGACCTGTGCTCTGTCATTCAGGCA
CAAGGTGACGGGCTCCTACCTGTCACACTTCAGGTTGGAGAAACACAGGTCGCCACGGAGCAGCTGTG
GGGAGGAAATGGTGGGCTAGGCTGGAGGAAACACAGATCACCTTGCAGGGCTGACATCAAGAGGAAATCACA
AAGATGATTAAAGGGTTGAAAAAAAGATCTATGTTGAAATTAAAGGAAACTGGGATTATTGAGCTGGAGAAG
AGAAGACTGAGGGCCAACATTGATGGTTCTCAAGTATATGAGGGTTGGCACAGAGGGTGGCAGCAGCTG
TCTCCATATGCAATAGAACAGAGGAAACTGGCTTAGACTAGAGTTAAAGGAGCATTCTGGCAG
GCCCATTTGAGAATCTCTCATAAAAAAAGATGTCGAAATCTCAGTATCTCTCTTCTTCTAAAAAATTAGA
AAAAAATTGTCATTTAAAGATGTTAAAGATGTTCTAACCAAGGAAAGTAAACAAATTATAGAATTTCACCAAA
AGATGTTGATCTACTAGTAGTATGTCAGTGGAAATCTTCTAGAATTAATTGAGCAAGGCTTAAATTAGG
CATTTCCCTCTGACCTCTAAATGGAGAGGAGTTGAAAGGGAGAGGCCACCAATGTCAGCTACTGAAATA
TCTCTCCCTATGGCAATCTAGGAGGAGTTGAAAGGGAAATCTTCTTAAATGAGGATGAGGATGAGGAC
AGATAATTAGTATCTCAGTAACTCTCTAGTGTGCGGTGTTCAATGTTCTCTATGGTAAAGGTTAAGCC
TTCTCCATATGTCATGAGATGTTCAAGATTTTTTTTAAAGAGATCTTCAAGGAACACAGTCAAGAG
ATTTCATCGGGTGCATTCTCTGCTCTGCTGAGCTGAGCTTCAAGGTTACCTGGCTCTGAGAAAGGCTGCCCTGG
ACACCCGGAGACCTTCTCCTACCTCATGAGTATGATTCTAGTCTCTCTTATCAATGGACTCTCCAGGTTCCAC
AGAACAGTAAATTTTGAAACATAGGCTACAATAGAAGGGCTCTCTGTCATTTAACTGTTAAAGGCAAGGGCTGG
AGGGGGAAATAATCATTAAGGCTTGTGAGTAACGGCGAAGATAATATGGCTGTAGATCTCATTTTAATGGTCTT
TCTCTTATGGTATATAACTGCAAGCTGAGGAGTAAAGGGAAATAATGAAATTCTACTTTCTGAGTGCACCA
TGATCATGCAACTAGTGGAGAAGTTACCAAGTACTGTTAATCATCTGTTTATTATTAATGTT
CTAAATAAAAAAATGTTAGTGGTTCCAAATGGCTAATAAAAACAAATTGTTGAAATAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSSLYLOAAAEEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQPRCKHGE
CIGPNKCKCHPGYAGKTCNQDLMNECGLKPRPKHRCMNTYGSYKCYCLNGYMLMPDGSCS
SALTCSMANCQYGCDDVVKGQIRCCPSPGLHLAPDGRCTVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLGQYC
CSSFARCYNVRGSGYKCKCKEGYQGDGLTCVYIPKV
MIEPSGPPIHPKGNGTILKGDGTGNNNWIPDVGSTWWPPKTPYI
PPIITNRP
TSKPTTRPTPKPTIPTPPPPPPLPTELRPLPPTTPERPTTGLTTI
APA
ASTPPGGITVDNRVQTDPQKPRGDVF
SVLVHSCNFHDHG
LCGWI
REKDNDLHWEPIRD
PAGGQYLTV
SAAKP
GGKA
ARLVLPLG
RLMHSG
GDLCLSFRHK
VTLHSG
GTLQV
FVRKHGA
GAALWGRNGGH
GWRQ
TQI
TRLGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

TTTCCATGGAAAGGATTATCACCTGTACAGGTTCTCTGCATTGCCCCCTTAGATGTGA
AATGTGGCTCAAGGTCTTACAACCTTCCATGGCTCAGAGGTAGGCCACTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA
CAAACTGCCAAATCTTACTGGCTCTGTGAATAAGTCTGTGGTTCTGACTTGGAAATACC
AACACAAGTTCACCATGATGCCACCCAAATGCATCTCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGGAAATGGAACCTCTATCTGCCAGTC
GAAGATAACAGTCACGGTTGATGATCTGTCAAAGCCAGTGGTGAGATTCACTCTCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGACTCGG
CTAGCTTACCATGGCTAAAAAATGGAGACCTGTCCACACAGCTCCACACTCTTTTC
TCCCCAAACAAATACCCCTCATATTGTCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCTGGTGAAGGAACCCATCTAGTGAATGGAAGGTGATCATTCATTATGCCCCATCATATTAT
GACACTTATGGCAACTTCAAGTGAATTCTGATAAAAGGGCTAAAGGTAGGGGAAGTGTTCATGT
TGACCTTGGAGAGGCCATCTTGTGATTGTTCTGTGATTCTCATCCCCCAACACCTACT
CTCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCTCTGCTTAGAAGTT
GCATCTGAGAAAGTGGAGGACTGACAATACTACATATATCATTAAGCATGGGCTCTGCTTAGAAGTT
CGGAGGAAAGGAAACTCATTGTCACCTTGTGAGTATACTGGAAATATCACTATTGGATT
CACAGAAAGGAAATCATTGTCACCTTGTGAGTATACTGGAAATATCACTATTGGATT
ATATCCATGTGCTCTTCTCTATGGAAAAAAATATCAACCTTACAAAGTTAAAACAGAA
ACTAGAAGGCAGGCCAACAGAAATACAGGAAAGGCTTACAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTGGAAATATATGAATTGTTGCTTTCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGATCGGGCAAGATTGCAAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGGACATCCAGAGT**TGA**ACTTTCATGG
GCTAACAGTACATTGAGTGAATTCTGAAAGAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAACTGGAATCAGTGAAGAAACCAGGACCAACACCTTACTCATTATTCTTACA
TCAGAAATAGAGGCATTATGCAAAATTGAACTTCAGGTTTTTCAGCATATAACAAATGTCCT
GTGCAACAGAAAACATTTGGGAAATATTCTCTCAGTGGAGAGTCCTCTCATCTGACGG
GGAGAACGAAAGTGCAGGGGTTCTCATAGTTTGTATGAAATATCTCTAACACCTCA
ATTAGTTCTACTCTACACTTCAACTATCATCAACACTGAGACTATCCCTGCTCACCTACAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTTGTTTATTAAATTTTTATTAGTG
TTAAGAATCTAAATTATGTTCAATTATTCTCAATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGTCACAAAACAAAATATGCCCTCTCTTTTTCAATCACC
AGTAGTATTGAGAGACTTGTAACACTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTCAAGGAAAGATGGATTCAAATAAAATTCTGTTTGTCTTTAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIOIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDPCSADSHPPNTYSWIRRTDNTTYIIKHGPLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDPGIYEVFVAPPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

TOP 1000 PROTEINS

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTCGCAGTTCCCCGGCAGTCTGGTGTGTT
GCTTGGGTGCTCCCTGGACGCACGGGCGGGAGCACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTCTGGAAAGGAGACTGGATGATGAGAATTATGCCCGTGGTGCCTGCT
TGTCAAATCTCAACCGGAATGGGAAAGTTTGCTGATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGCAGCAGGACTGAGCTGGACGGTTTATCATAACTGCTC
TTCCTATTTATCATGTAAAAGATGGTATTAGGCGTATCAGGGTCCAAGGACTAAAG
AAGGACTTCATAAACTTTATTAAGTGAAAAGACTGGAAAGAGTATTGAGCCGTTTATCATG
GTTTGGTCCAGGTTCTGTCGTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGGA
TCAGGACGTGCCCATAACTTTATTAAGGACCTGGATGGCAGTGTGGGATCATATACT
GTTTGGTCCGTGAACTCTGTTTCCGGATGTTATTAGGACTCTGTGATGATATTTGGC
AGATTGCCTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAACTGCAACCTTTGAAAAAGTGGAGGAGAACAGGCGGATGAAAGAA
GATGTTCTCAGAGAAGAAGCTGAAAGTAAAGGAACAAACAAAGACTTCCACAGAATG
CATAAGACAACGCTCTCGGGTCCATCATGGCCACAGATAATCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTGATAAAACAGAAGATTGATCATTTGTTTGGTTAAGGT
AACTGTGACTTTTGATATTGCAAGGTCAGTCTGATGTTGCATTAAATTGAAAGACTA
CATTCGAGACATAAAGCACTAGGTATACAGTTTGAAAATGATGATTAAGCACAGTATG
GTTTAAATAGTCTCTATTTTGAAAAATCGTGCCAAGCAATAAGATTATGATATTTGT
TTAATATAACCTATTCAAGTCTGAGTTTGAAAATTACATTCCCAGTATTGCATTAT
TGAGGTATTTAGAAGATTTTAGAGAAAATATTCTCATTTGATAATTTCTCTG
TTTCACTGTGAAAAAAAGAGATATTCCCATAAATGGGAAGTTTGCCATTGTCTCAG
AAATGTGTATTTCAGTGACAATTCGTGGCTTTTAGAGGTATTCAAAATTTCTGT
ATTTTAGGTATGCACTAAAAACTACCTTTACATTAATTACAGTTTTCACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAGTTCATGGTATTCTCTTGT
CAACAAAGTTGATTCTCTGTATTTTCTACTTACATGGGTACTTTTTATTTT
CAAATGGATGATAATTCTGGAAACATTTTATGTTAGTTAGTAAACAGTATTTTTTG
GTTTTCAACTGAGTTACTGAGAGATCCATCAAAATTGAAATCTGTGTAATTTTAAATT
TTGGCCACTTTTTGATGTGGAAGGTGAACATTCTGATTTTGTCTGTGAAAAGCCTTGGTA
TTTACATTTGAAAAAGGCTTAATTTGAAAGTTTGCATTCTACTCAGGAAAAG
CATCTTCTGTATATGCTTAAATGTTTGTCTCATACAGAAAGTCTTAATTGAT
TTACAGTCTGTAATGCTGATTTTAAAAACATTTTTTATGTTAAAGACAA
ACTTCTGATATTACCTGTGTTCTTCTGACTGGTAATATTGGTCTGGGATTTCACAGAAAA
GTCAGTAGGATGGAACATTTAGTGTATTCTACTCTTAAAGAGCTAGAAATCAGTTTT
CACCTTAAAGAAGGGGGAAATCAAAATACAATGAATCAACTTGACCATTACGTAGAC
AATTCTGTAATACAGTTCTTAAAGCCCTCCTCTGAGCTGTTGCTGTGAAATCCATTAGATTACAG
TATCGTAATACAGTTCTTAAAGCCCTCCTCTGAGCTGTTGCTGTGAAATCCATTAGATTACAG
AAAGAGTTGATGTCTAACTTGTGTATGCCTTAGAAAATCTCTAACGACAAAATAAAC
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGHRRSNVRVITDENWRELLEGDWMIIFYAPWCACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GGCAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAACCGCAAGCAGTGTGACACTTCCCTGTGACC~~AT~~GAAACTCTGGGTGCTG
AAGTCCTGCCCCAGAGCAGTGTGACACTTCCCTGTGACC~~AT~~GAAACTCTGGGTGCTG
ATTGCTGATGGCTGGTTGGTCTGAGCTGTGCAAGGCCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGCAGTCTGAAAGAGTACATC
CTTGAGGGAAAGCCAAGCTTCAAGATAAGAGCTGGCCAACAAAATGAAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCGTGAATGCTCACAAACTGG
TGAAGCGGCTAACACACAGACTGGCTGCGCTGGAGGACCTTGTGCAAGGACTCACGTGCA
GGTTTATGCCAACCTCTGTGAGGAACTTCAAGGACACATACAGGGCTGGACCCAGGCACAAATTCCA
AGCTGCCAACGCCCTGATGAGAACTTCAAGGACACATACAGGGCTGGACCCAGGCACAAATTCCA
GAGGGGAACTTCAAGGACCAAGTACCAAGGAATGCTGAGTGTGGATGACTGCTTTGGATG
GGCGCTCGGCCATAATGAGGGGACTTATTCATACAGGTGTTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGGAGGCCACCAAACCAAGTACAGGTGCTGGACTAACCTCA
GCTATGCTGCTTCCAGTGGGTGATCTGACCGTGCCCTGGAGCTCACCCGCCCTGCTC
TCCCTGTGACCCAAAGGCCACGAGCTGGAGGAATCTGGCTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAAAAGTAAACAATCAGACAGAACCTGAGCTTACCAACCCCAGAGGCA
TCTATGAGGCCCTGTGAGACTACCTGCTGAGAGGGATTTACGAGAGCCTGTGCTGGG
GAGGGTGTCAAACGTGACACCCGTAGACAGAAGAGGCTTCTGAGGTACCCACATGCCAA
CAGGGCCCCAAGCTGCTCATGGCCCTTAAGAGGAGGAGCAGTGGGACAGCCCGCACA
TCGGTCAAGGACTACAGTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGCACGAGCCACCGTGTGATCCAAGACAGGAGTCTCACTGTGCCAGCTA
CCGGTTTCCAAAAGCTCGGCTAGAGAAGATGATGACCCCTGTTGTGCCCGAGTAATC
GTCGGATGAGCATATCACAGGTTAACAGTAAAGACTGAGAATTGTTACAGGGTCAAAT
TATGGAGTGGGAGGACAGTATGAAACCGCATTGCACTTCTAGGGCACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGGCACTTCTTAACTACATGAGTGTAGAAGCTG
GTGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACACCTCTGGGAGGGAGGGAAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTGTGGGCTGCAAGTGGTCTCCATAAGGTTCCATGAACGAGGACAGGGATTCT
TGAGACCTTGTGGATCAAACAGAAGTGTGACT~~G~~ACATCCTTTCTGCTCTCCCTTCTGGTC
CTTCAGCCCATGTCACAGTGCAGACAGAACCTTGTATGTTCTGGAGCAGAGGGAGACCA
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCAACTAGGGGACTCTGT
GTGACTGAACTCCAGGCCCTCCATTGAGCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AACTGGCTGAGCAGAGTTAGCTGTAGGCCCTAGCAAGGTGCCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCTGAAACAAAGTTCTGATACCTGTTACATGTTGTTTAT
GCCATTCTATCTATTGTGGTTACAAAAAATGCTCCCTACAGGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSVCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFF
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLSSLDPSHERAGGNLR
YFEQQLLEEEERKTLTNQTEAELATPEGIYERPVDFYLPERDVYESLCRGEVVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHI VRYYDVMSEBEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYSMSDEVEAGGATVFPDLGAIWPKKGTAVFYWNLRSGEVDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,

346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCCTTTAGTGGAGACAGAACCAATCCCAGTGTGAGTGAAATTGATTG
TTCAATTATTACCGTTTGCCTGGGGTTAGTCGACACCTTCACAGTGAAAGCAGCAGAACGGAGTTGGA
AGACAGGACAATCTCTTGGGGATGCTGGCTCGGAAGGCCAGCGGGGCTGTCTGTCTTGCCCATGACCC
CAGGTTCTCTGTTAAACTGAAGGCCTACTAGGCTTGGTGGCCCATCAATCCATTGATCCTTGAGGGCTGTG
CTGGGGCACCCACTGGCAGGCCATCACCATGCGACTGAGTCCTGTGGCTCTGCTGCCAGGGCTTC
CCCCATCTTAAAGGCTGTCCTGGGGTGAAGGGAGCAGAGGCCACAGAATTCAGATTCGAGAGCTCGGTAG
ATGAAGACTTCAAACCCGGATTGTCCTACTACAGGGACCCCAACAGGCCATAAGAAGGTGTCAGGACTC
GTACATCCAGACAGAGCTGGGCTCCGGTGGAGCGCTGGCTGACCTCCCGAGGCTACACTGTCCA
CTTGCCCTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGGTACTCTACTTCACTGGCAGGGGG
CCCCGGCTCCAGCAGGGATGCAAGGTGTCCTAGGGGATGAGCGGCCCTGGCTCATGTGAGAACCTG
GCCACCTTCAACACACTTGGGGCCGACTGACTGTTTCTCATGAGGATGACACATATGCGAGGCC
CCCGCTGGCAGCCCTGCGCACCTCAGCATCACCAAGACACTGTACTAGGCCAGAGGAGTTCATG
GCCAGGAGCAGGGCTGGCTCCGGAGGACATTCAGCTGGCTTGGGACTACCTGGTGTGACCGAGTCTCTG
GCCACATCTGGATGCTGGCTCCGGAGGACATTCAGCTGGCTTGGGACTACCTGGTGTGACAGTGGCTTGG
GCCAGGAGCAGGGCTGGCTCCGGAGGACATTCAGCTGGCTTGGGACTACCTGGTGTGACAGTGGCTTGG
ACTCTCTGGGCGTGGCTGGTCTACAGCAGGGGCGACTGAGCTGGCTTGGGACTACCTGGTGTGACAGTGG
ACCCCTGAGAAAGGAGGGAGCTGGCTCCGGAGGAGCAGACTGGCTTGGGACTACCTGGTGTGACAGTGG
ACCCGGCTTACACAAACGCTCAGCCCTGGAGTTGAGCAGGGCTTAAGTGAACAACTGCGAGGCTCAGA
TCCGGAAACTTGCACCTGGCTGGAGGGGGAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CACCAACACTCCGCTTGGGACTCTTCAAGAGCAGCACACCTTCTCTGTCAGATGGGG
CTCCAAGTGGCCACTACAGGGGGTAGCAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
ATCAGGGGCTTACAGGCCCGCTCGCTTCAAGAGCAGCAGACTCTAACAGGGCTATCGCGCTTGG
GGGGCATGGAGTACACCCCTGGAGCTGGTGTGGAAATGTGACACAGGGTGGGACCCGGCCTGGCTC
GGGGCATGGAGTACACCCCTGGAGCTGGTGTGGAAATGTGACACAGGGTGGGACCCGGCCTGGCTC
AGCTGGTGTGCCACTCTGGTGTGAGAACCTGACTGAGCCCGGCTTCTGAGGGCTTGGCAGGCAATGTCC
TGGAGCCACGAGAACATGCAATTCTCACCTGGTGTGGCTGGCTAACGGGCCACAGAGAGGTGGCGTGGAGCTCAG
ACCCATTCTGGGTGAAGCTGCAAGCAGGGAGTGAAGCAGCGTACCTGGGACAGGCTGGCTTGGCTCG
CTGTGGAGCAGGGCCCCCTCCAGGTGGACTCATGGACGGTGTGCAAGAAGCACCCCTGGACACTCT
TCTTCTTACACCGTGTGGACACCCCTCCCTGGTGTGACCCCTCCGGGGGGCTCTATAGGGGGAGATTG
GGCAGGGCTTACAGGAGTCAACCTGGCTGCAAGGAGTCAACCTGGCTGACAGAGATACCCCAAGGGCCC
CGGGGGCTGGCCCTGACCCCTGGTGTGGAAATCTACCTATGTGACTGAGGCCACCCGGTGC
ACCCGGCAGGCTTCTGGGGAGGTGTCTCACAGCTGACTCTGGGGCCGAGGGCTGGCAGGTGAC
TGGCAGGGCAGGAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
ACCTCTTCTGGGGCGTAGAGGCCAGGGCTGGTGCAGAAGTTCTCTGGAGAGCTGAGGCCACGGCTCAGTGAAG
AACTCTACACCCGCTGCCGCTCGAACCTGGAGGGCTAGGGGGCGTGCCGAGCTGGCTATGGCTCTTGT
ACGAGGAGCAGGCCATAGGACTTAAGCCGCTGGGGCCCTAACCTTACACCTTCTTGTCTGCCAGCC
CCAGGAAGGGCAGGGCAAGATGTCAGAGATAGAGAATTTGTGCTTAAATATGAAAGTATTAA
ACATGCTCTGTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEFKPRIVPYYRDPNPKVVLTRYIQTTELGSRERLLVAVLTSRATLSTLAVVNRTV
AIHHFPRLLYFTQORGARAPAGMQVVSHGDERPAWLMSETLRHLHHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSRLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPSPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQGASRADVGDALETALEQLNRRYQPLRFQKQRLLNGYR
RFDPARGMEYTDLLLLECVTQRGHRRALARRVSLLRPLSVEILPMPYVTEATRVQLVLPPLL
VAEAAAAPAFLEAFAAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKA AAAAE LERRYPG
TRLAWLAVRAEAPSQVRLMDVSVSKHPVDTLFFLTWTRPGPEVLRNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELACQEEEAALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAACCCGTGCGCGCTGCGCTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG
AACGATTTCTGTCTTGACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAAGAAGATATCTTGAAGAAATTCA
GAGGATGAGCGCATGGAGCTAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTTGGACCAAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATCGCCTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCCITGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACGCCCTCTATCAGGCCACACTATAAAATCTGGAGACCTGAAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAATCAATGAAAAGACTTAACGCCCTCT
CAATATCCCAGAAAAGTGTCTGAAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAAGATGCTGATGGA
AAAGATGTATTAATACCAAACTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCCAGGTAGTAGAAGGCTTGTTCAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTTAGGGCATTGGGATATTTCAT
GATGCATTGGTTTCTTACCTCCAAATGGCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTTGTCATTATTGTTAGTAGTAACTACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAAATAACTTAAATAATTATAT
GTGATAAAATTCTAAATTATGAAACATTAGAAATCTGTGGGCACATATTGCTATTGGTT
AAAAAAATTAAACAGGTCTTAGCCTCTAAGATATGCAAATGATATCTCTAGTTGTAATT
TGTGATTAAGTAAACATTGTTAGCTGTGTGTTCCCTTACTCTAAACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGTGAAAAAT

FIGURE 120

MLSSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIIILVKPKDVSILWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNMWMRKA
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYLFLKKDPSPQFYLGHТИKSGDLEYVGMEGG
IVLVSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGCGTCGATCTTACCAACAAAACACTCCTGAGGAGAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAAATGAATTCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTCTTCCCAAATGTTCTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCTGTTCATCACAGATGTGTTGTGACATTGCGAT
CTTCAAAACCTGTGATGAGAAAAGTTCACTGAGAATTTCACAGAGCTCTCTGCT
ACAATTATGGATCAGGTTCACTGACACCATTCTGGCGTTAACGTTAAAGAACTGTCAGC
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCGAGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGGATGTAGGGAGCCAAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTCGGATTGAAATGGTAGGAATAATCCTTGA
AACAAAGGAAAATCTCTTAAGAACAGAACAGGACAACACTCAAATGTGTAAGAAGGAAGAGCA
AGAACATGGCACACCCACCGCCCCACAGAGAAATTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPIFLSACFITRCVVTFRIFQTCDEKKFQLPEN
PTELSCYNYGGSVKNCCPLNWEIFQSSCYFFSTDТИSVALSLKNCSAMGAHLVVINSQEEQ
EPLSYKKPKMREFFIGLSDQVVEGQWQWDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPCKRVPKAAPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQQYCIAASNDAGSARCEEQEMEVYDLDNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267